

Figure 1: antibody titer in broilers (actively vaccinated with intermediate vaccine at 3 weeks)

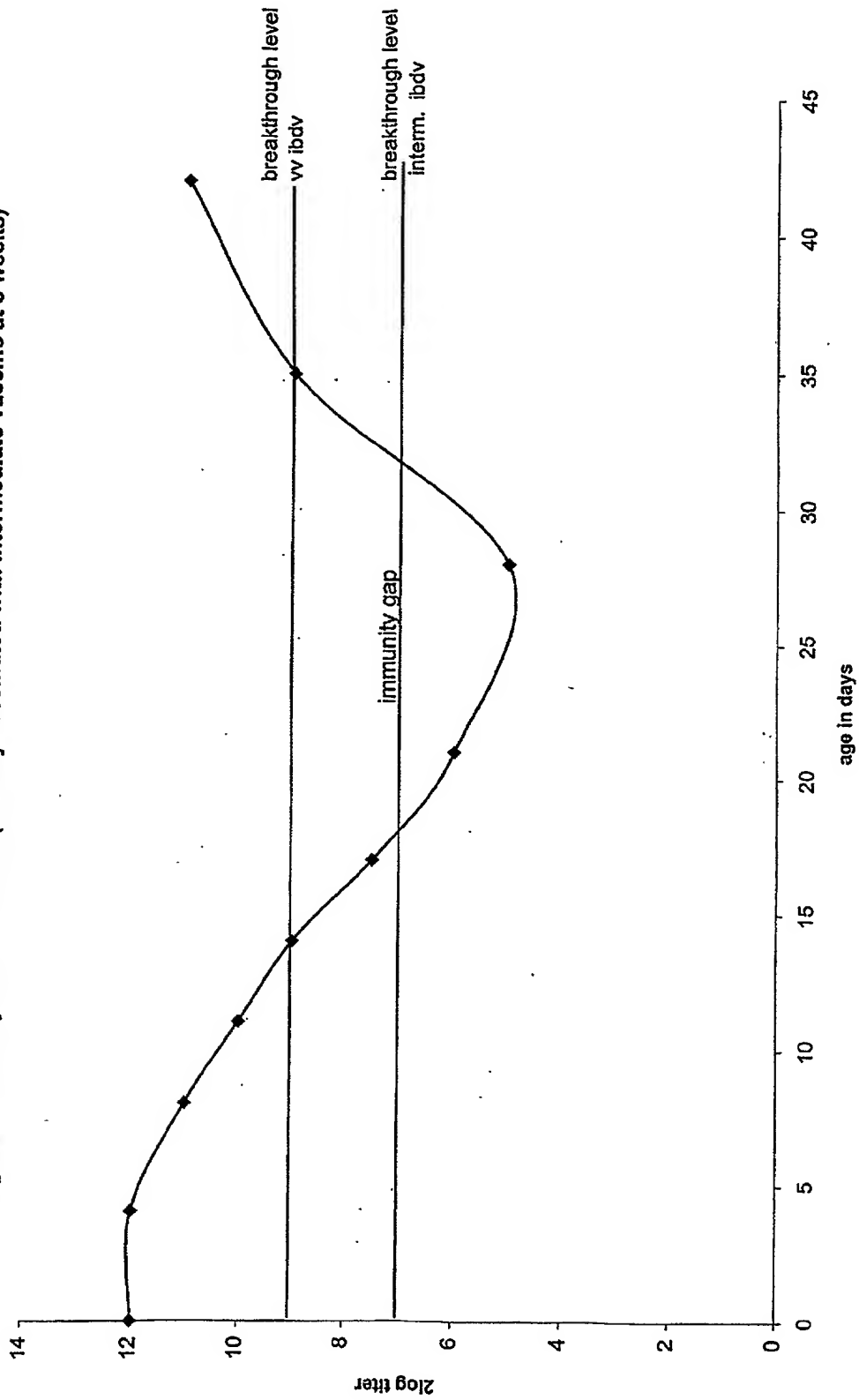


Fig.2a Alignment of IBDV A-segment cDNA sequences

Consensus	GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCGWCAA GGYCTTGTTC CAGGATGGAA CTCCT	75
CEF94-AC.T.....T.....	75
D6948-AT.A.....C.....	75
TY89-A	-----	
Consensus	CCTTCTACAA YGCTATCATT GATGGTYAGT AGAGATCAGA CAAACGATCG CAGCGATGAC RAACCTGCAA GATCA	150
CEF94-AC.....C.....A.....	150
D6948-AT.....T.....G.....	150
TY89-A	-----	
Consensus	AACCCAAACAG ATTGTTCCGT TCATACGGAG CCTTCTGATG CCAACAACCG GACCGGCGTC CATTCCGGAC GACAC	225
CEF94-A	225
D6948-A	225
TY89-A	-----	
Consensus	CCTRGAGAAG CACACTCTCA GGTCAGAGAC CTCGACCTAC AATTGACTG TGGGGGACAC AGGGTCAGGG CTAAT	300
CEF94-A	...G.....	300
D6948-A	...A.....	300
TY89-A	-----	
Consensus	TGCTTTTTC CCTGGWITCC CTGGCTCAAT TGTGGGTGCT CACTACACAC TGCAGAGCAA TGGGAACCTAC AAGTT	375
CEF94-AA.....	375
D6948-AT.....	375
TY89-A	-----	
Consensus	CGATCAGATG CTCCTGACTG CCCAGAACCT ACCGGCCAGY TACAACCTACT GCAGGCTAGT GAGTCGGAGT CTCAC	450
CEF94-AT.....	450
D6948-AC.....	450
TY89-A	-----	
Consensus	AGTGAGGTCA AGCACACTYC CTGGTGGCGT TTATGCACTA AAYGGCACCA TAAACGCCGT GACCTTCCAA GGAAG	525
CEF94-AT.....C.....	525
D6948-AC.....T.....	525
TY89-A	-----	
Consensus	CCTGAGTGAA CTGACAGATG TTAGCTACAA TGGGTGATG TCTGCAACAG CCAACATCAA CGACAAATY GGGAA	600
CEF94-AT.....	600
D6948-AC.....	600
TY89-A	-----	
Consensus	CGTCCTAGTA GGGGAAGGGG TMACCGTCCT CAGCTTACCC ACATCATATG ATCTTGGGTA TGTGAGRCTY GGTGA	675
CEF94-AC.....G..T.....	675
D6948-AA.....A..C.....	675
TY89-A	-----	
Consensus	CCCCATTCCC GCWATAGGGC TYGACCCAAA AATGGTAGCM ACATGTGACA GCAGTGACAG GCCCAGAGTC TACAC	750
CEF94-AA.....T.....C.....	750
D6948-AT.....C.....A.....	750
TY89-A	-----	
Consensus	CATAACTGCA GCCGATGATT ACCAATCTC ATCACAGTAC CAACAGGTG GGGTAACAAT CAACTGTTC TCAGC	825
CEF94-AC.....	825
D6948-AG.....	825
TY89-A	-----	
Consensus	YAAIATYGAT GCCATCACAA GCCTCAGCRT YGGGGGAGAR CTCGTGTTTC AAACAAGCGT CCAMGGCCTT RTACT	900
CEF94-A	C..C..T.....G..T.....G.....C.....G.....	900
D6948-A	T..T..C.....A..C.....A.....A.....A.....	900
TY89-A	-----	
Consensus	GGGYGCIACC ATCTACCTYA TAGGCTTTGA TGGGACWCG GTAATCACCA GRGCTGTGGC CGCARACAAT GGGCT	975
CEF94-A	...C..C.....C.....A.....G.....A.....	975
D6948-A	...T..T.....T.....T.....A.....G.....	975
TY89-A	-----	

20470-7-99-001

Fig.2a Contd. Alignment of IBV A-segment cDNA sequences

Consensus	RACGRCCGGC	ACYGACAACC	TTWTGCCATT	CAATMTTGTG	ATTCCAACMA	RCGAGATAAC	CCAGCCAATC	ACATC	1050
CEF94-A	G...A.....	..C.....	..T.....C.....A..	A.....	1050
D6948-A	A...G.....	..T.....	..A.....A.....C..	G.....	1050
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	CATCAAACTG	GAGATAGTGA	CCTCCAAAAG	TGGTGGTCAG	GCRGGGGATC	AGATGTCRTG	GTCRGCAGW	GGGAG	1125
CEF94-AA.....G..	...G....	A.....	1125
D6948-AG.....A..	...A....	T.....	1125
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	CCTAGCAGTG	ACGATCCAYG	GTGGCAACTA	TCCAGGGGCC	CTCCGTCCCG	TCACRCTAGT	RGCTTACGAA	AGAGT	1200
CEF94-AT.....G..	G.....	1200
D6948-AC.....A..	A.....	1200
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	GGCAACAGGA	TCYGTGTTA	CGGTGCGCYG	GGTGAGCAAC	TTCGAGCTGA	TCCCAAATCC	TGAAGTACGA	AAGAA	1275
CEF94-AC.....T..	1275
D6948-AT.....C..	1275
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	CCTGGTYACA	GAATACGGCC	GATTGACCC	AGGAGCCATG	AACTACACAA	AATTGATACT	GAGTGAGAGG	GACCG	1350
CEF94-AT...	1350
D6948-AC...	1350
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	TCTTGGCATC	AAGACCGTMT	GGCCAACAAG	GGAGTACACT	GACTTTCGYG	ARTACTTCAT	GGAGGTGGCC	GACCT	1425
CEF94-AC..T..	A.....	1425
D6948-AA..C..	G.....	1425
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	CAACTCTCCC	CTGAAGATTG	CAGGAGCATT	YGGCTTCAA	GACATAATCC	GGGCCMTAAG	GAGGATAGCT	GTGCC	1500
CEF94-AC..A..	1500
D6948-AT..C..	1500
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	GGTGGTCTCY	ACAYTGTTC	CACCYGCCGC	TCCCCTAGCC	CATGCAATTG	GGGAAGGTGT	AGACTACCTG	CTGGG	1575
CEF94-AC...	..T.....	..T.....	1575
D6948-AT...	..C.....	..C.....	1575
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	CGATGAGGCA	CAGGCTGCTT	CAGGAAGTGC	TCGAGCCGCG	TCAGGAAAAG	CAAGAGCTGC	CTCAGGCCGC	ATAAG	1650
CEF94-A	1650
D6948-A	1650
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	GCAGCTRACT	CTCGCCGCG	ACAAGGGGTA	CGAGGTAGTC	GCGAATCIRT	TYCAGGTGCC	CCAGAATCCY	GTAGT	1725
CEF94-AG...A..	C.....C...	1725
D6948-AA...G..	T.....T...	1725
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	CGACGGGATT	CTYGCCTCAC	CTGGGRTACT	CCGCGYGCA	CACAACCTCG	ACTGCGTGT	RAGAGAGGGT	GCCAC	1800
CEF94-AT...G...T...A..	1800
D6948-AC...A...C...G..	1800
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	GCTATTCCCT	GTGGTYATYA	CGACASTGGA	AGAYGCCATG	ACACCCAAAG	CAYTGAACAG	CAAAATGTTT	GCTGT	1875
CEF94-AT..T.C.....T.....	1875
D6948-AC..C.T.....C.....	1875
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	
Consensus	CATTGAAGGC	GTGCAGAGA	AYCTCCAACC	TCCWTCTCAA	AGAGGATCCT	TCATACGAAC	TCTCTCYGGA	CAYAG	1950
CEF94-AC.....	..T.....T..	..C...	1950
D6948-AT.....	..A.....C..	..T..	1950
TY89-A	-----	-----	-----	-----	-----	-----	-----	-----	

204770-729400T

Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Consensus	AGTCTATGGA TATGCTCCAG ATGGGGTACT TCCACTGGAG ACTGGGAGAG AYTACACCGT KGTCCCAATA GATGA	2025
CEF94-A	2025
D6948-A	2025
TY89-A	
Consensus	TGCTCTGGGAC GACAGCATTG TGCTGTCCAA AGAYCCCATG CCTCCTATTG TGGGAAACAG YGGAAAYCTA GCCAT	2100
CEF94-A	2100
D6948-A	2100
TY89-A	
Consensus	AGCTTACATG GATGTGTTTC GACCCAAAGT CCGMATCCAT GTGGCYATGA CGGGAGCCCT CAAYGCYTRT GGCGA	2175
CEF94-A	2175
D6948-A	2175
TY89-A	
Consensus	GATTGAGAAM GTRAGCTTTA GAAGCACCAA GCTCGGCACT GCACACCGAC TTGGCCCTYAA GTTGGCTGGT CCCGG	2250
CEF94-A	2250
D6948-A	2250
TY89-A	
Consensus	WGCATTYDAY GTRAACACCG GGYCCAACG GGCACGCTT ATCAAACGTT TYCCTCACA TCCMCGMGAC TGGGA	2325
CEF94-A	2325
D6948-A	2325
TY89-A	29
Consensus	CAGGYTMCCY TACCTCAACC TWCCMTAYCT YCCACCMAMW GCWGGACGYC AGTWC SAYCT KGCCMTGGCH GCHTC	2400
CEF94-A	2400
D6948-A	2400
TY89-A	104
Consensus	MGAGTTCAAA GAGACCCCMG AACTCGARRR YGCGTSMGW GCMATGGAMG CWGCGCMMAA CGTSGACCCA YTRTT	2475
CEF94-A	2475
D6948-A	2475
TY89-A	179
Consensus	CCRMTCWCD CTCMRBTST TCATGTGGYT GGAAGARAAY GGGATTGTRA CYGAYATGGC YAACTTCGCM CTCAG	2550
CEF94-A	2550
D6948-A	2550
TY89-A	254
Consensus	CGACCCGAAC GCMCAYMGGA TGMRAATTY YCTHGC AAAY GCWCCMCARG CMGGHAGCAA GTCGCARAGR GCCAA	2625
CEF94-A	2625
D6948-A	2625
TY89-A	329
Consensus	GTAYGSSACR GCWGGCTACG GASTGGAGGC YMGRGGCCCC ACDCCAGARG ARGCACAGAG GGARAAAGAC ACACG	2700
CEF94-A	2700
D6948-A	2700
TY89-A	404
Consensus	GATCTCAAG AAGATGGARA CBATGGGCAT CTACTTYGCA ACACCRGAAT GGGTAGCACT CAAYGGGCAC CGRGG	2775
CEF94-A	2775
D6948-A	2775
TY89-A	479
Consensus	SCCAAGCCCC GGCCAGCTVA AGTACTGGCA RAACACAMGA GAAATACCDG AHCCMAACGA GGACTAYCYA GACTA	2850
CEF94-A	2850
D6948-A	2850
TY89-A	554
Consensus	YGTGCAYGCR GAGAAGAGCC GGTGGGCTC AGAAGAACAR RTCYTAAGGG CAGCYACGTC GATCTACGGG GCTCC	2925
CEF94-A	2925
D6948-A	2925
TY89-A	629

Fig.2a Contd. Alignment of IBDV A-segment cDNA sequences

Consensus	AGGACAGGCW GARCCACCCC AAGCYTTCAT AGACGAAGTY GCCARRGTCT ATGAAATCAA CCATGGRCGT GGYCC	3000
CEF94-AA ..G..... ..T..... ..T....AA..... ..A... ..C..	3000
D6948-AA ..G..... ..C..... ..C....AA..... ..G... ..C..	3000
TY89-AT ..A..... ..C..... ..C....GG..... ..G... ..T..	704
Consensus	MAACCARGAR CAGATGAARG AYCTGCTCYT GACTGCGATG GAGATGAAGC ATCGCAATCC CAGGCGGGCT CYACC	3075
CEF94-A	A.....A..AA. .T.....T.T...	3075
D6948-A	C.....A..AA. .T.....C.C...	3075
TY89-A	A.....G..GG. .C.....C.C...	779
Consensus	AAAGCCMAAG CCAAAACCCA ATGCTCCAWC ACAGAGACCC CCTGGWCGGC TGGGCGGCTG GATCAGGRCB GTCTC	3150
CEF94-AC...A.T..... ..A.C	3150
D6948-AC...A.T..... ..G.T	3150
TY89-AA...T.A..... ..A.G	854
Consensus	TGAYGAGGAC YTKGAGTGAG GYNCTGGGA GTCTCCCGAC ACCACCCGCG CAGGYGTGGA CACCAATTMR KMMHT	3225
CEF94-A	...T..... C.T..... .TA..... ..T..... ..CG GACT.	3225
D6948-A	...T..... C.T..... .CT..... ..C..... ..CG GCCA.	3225
TY89-A	...C..... T.G..... .CT..... ..T..... ..AA TCAC.	929
Consensus	ASWRMATYCS AAATTGGATC CGTTCGCGGG TCCCC	3260
CEF94-A	.CAAC..C.C	3260
D6948-A	.CAAC..C.C	3260
TY89-A	.GTGA..T.G	964

Fig.2b		Alignment of IBV B-segment cDNA sequences	
Consensus	GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGYGATRM CCRCCGCTRG CTGCC	75	
CEF94-BC...AA ..G....G.	75	
D6948-BT...GC ..A....A.	75	
Consensus	ACGTTAGTGG CTCCTCTTCT TGATGATTCT RCCACCATGA GTGACRTTTP CAAYAGTCCA CAGCGCGGAA GCAMG	150	
CEF94-BG..... ..A.... ..C..... ..C.	150	
D6948-BA..... ..G.... ..T..... ..A.	150	
Consensus	ATMTCAGCAG CGTTCGGCAT AAAGCCTACW GCTGGACARG AYTGGAAGA ACTCYTGATC CCTAARGTYT GGGTG	225	
CEF94-B	..C..... ..T..... ..A.... ..C..... ..T..... ..A..T.	225	
D6948-B	..A..... ..A..... ..G.... ..T..... ..C..... ..G..C.	225	
Consensus	CCACCTGAGG ATCCSYTKEG CAGCCCTAGT CGWCTGGCMA AGTTCCTCAG RGARAACGGC TACAARRPTY TGCAG	300	
CEF94-BGC..T.. ..A.... ..A.... ..A..G..... ..AG..T.	300	
D6948-BCT..G.. ..T..... ..C..... ..G..A..... ..GA..C.	300	
Consensus	CCACGGTCTC TRCCYGAGAA TGAGGAGTAT GAGACCGAYC AAATACTCCC WGACYTAGCW TGGATGMGRC AGATA	375	
CEF94-BG..C..... ..C..... ..T..... ..A.... ..A.... ..C..A.	375	
D6948-BA..T..... ..T..... ..T..... ..C....T.A..G.	375	
Consensus	GARGGRGCTG TTTTAAACC MACYCTATCT CTCCTCYATTG GAGAYCAGGA GTACTTCCW AARTACTACC CAACA	450	
CEF94-B	..A..G.... ..C..T..... ..T..... ..T..... ..A.... ..G..... ..A....	450	
D6948-B	..G..A.... ..A..C..... ..C..... ..C..... ..T..... ..A.... ..A....	450	
Consensus	CAYCGCCCKA GCAAGGARAA GCCCAATGCG TACCCGCCMG AYATCGCAYT ACTCAAGCAG ATGATYTACY TGTIT	525	
CEF94-B	..T....T.G.... ..A.... ..C....C.T....C.	525	
D6948-B	..C....G.A.... ..C....T.C....T.C....T.	525	
Consensus	CTCCAGGTTC CMGAGGCCAM MGAKRRCTW AARGATGARG TMACCTMYT RACCCAAAC ATWAGRGAYA ARGCC	600	
CEF94-BA.....A C..GGG...A ..G....A. ..A....CT. G..... ..A..G..C. ..G....	600	
D6948-BC.....C A..TAA...T ..A....G. ..C....AC. A..... ..T..A..T. ..A....	600	
Consensus	TAYGGRAGTG GGACCTACAT GGGACARGCM ACYMGACTTG TKGCTATGAA RGAGGTGCCC ACTGGRAGAA ACCCA	675	
CEF94-B	..T..A.... ..A....A ..TC..... ..G..C.... G....C.... ..A.... ..A....	675	
D6948-B	..C..G.... ..G....C ..CA..... ..T..T.... A....T.... ..G.... ..G....	675	
Consensus	AACAARGATC CTCTAAGCT TGGGTACACY TTTGAGAGCA TMGCSAGCT ACTTGACATC ACWYTACCGG TAGGC	750	
CEF94-BG.... ..T..... ..C..G.... ..AC..... ..TT.....	750	
D6948-BA.... ..C..... ..A..C..... ..A..C..... ..TT.....	750	
Consensus	CCACCCGGTG AGGATGACAA GCCCTGGGTR CCACTCACAA GRGTGCCGTC AMSGATGTTG GTWCTGACGG GAGAC	825	
CEF94-BG..... ..A..... ..C..... ..A..... ..A....	825	
D6948-BA..... ..G..... ..A..... ..T..... ..C....	825	
Consensus	GTAGATGGSG AMTTTGAGGT TGARGAYTAC CTTCCCAAAA TCAACCTCAA GTCATCAAGT GGACTRCCMT ATGIW	900	
CEF94-BC..C..... ..A..T.... ..A..... ..A..A.... ..A....	900	
D6948-BG..A..... ..G..C.... ..A..... ..G..C.... ..T....	900	
Consensus	GGTCGCACCA AAGGAGARAC WATTGGSGAG ATGATAGCYA TMTCAACCA GTTCTYMSA GAGCTATCAR CRCTG	975	
CEF94-BG..A.....C.... ..T....C..A.... ..CA.... ..A..A....	975	
D6948-BA..T....G.... ..C....A..G.... ..TC.... ..G....G....	975	
Consensus	YTGAAGCARG GTGCAGGGAC AAARGGGTCR AACAGAAGA AGCTRCTCAG CATGYTAAGT GACTAYTGGT ACTTA	1050	
CEF94-B	T.....A.G....AA..... ..T..... ..T.....	1050	
D6948-B	C.....G.A....GG..... ..C..... ..C.....	1050	
Consensus	TCATGYGGGC TTTTGTTC C NAAGGCTGAR AGGTACGACA AAAGYACATG GCTCACCAG ACCCGKAACA TATGG	1125	
CEF94-BC.... ..A.....AT..... ..G....	1125	
D6948-BT.... ..C.....GC..... ..T.....	1125	
Consensus	TCAGCTCCAT CNCCAACACA CCTCATGATC TCWATGATMA CCTGGCCCGT GATGTCCAAY AGCCCAAYAA ACGTG	1200	
CEF94-BC..... ..T....C.C..... ..T.....	1200	
D6948-BA..... ..A....A.T..... ..C....	1200	

Fig.2b Contd. Alignment of IBDV B-segment cDNA sequences

Consensus	TTGAACATG ARGGGTGTC RTCACTCTAC AARTTCAACC CGTTYAGAGG WGGGYTRAAC AGGATCGTSG AGTGG	1275
CEF94-BA.....A.....A.....C.....A...T.G... ..C.....	1275
D6948-BG.....G.....G.....T.....T...C.A... ..G.....	1275
Consensus	ATATWGGCYC CGGAWGAACC CAAGGCYTW GTATATGCKG ACAACATATA CATGTGYCAC TCMACACGT GGTAC	1350
CEF94-B	...T...C... ..A..... ..TC.TG..... ..C... ..A.....	1350
D6948-B	...A...T... ..T..... ..CT.AT..... ..T... ..C.....	1350
Consensus	TCAATGACC TAGAGAAGGG TGAGGCAAAC TGCACKCGYC AACACATGCA RGCCGCMATG TACTACATHC TYACC	1425
CEF94-BT.C..... ..A...A... ..A... ..C...	1425
D6948-BG.T..... ..G...C... ..C... ..T...	1425
Consensus	AGAGGRTGCT CMGAYAACGG YGACCCMATG TTCAATCARA CATGGGCCAC CTTTGCSATG AACATTGCCC CWGCT	1500
CEF94-BG.... ..A..C.... ..C....A... ..A..... ..C.... ..T...	1500
D6948-BA.... ..C..T.... ..T....C... ..G..... ..G.... ..A...	1500
Consensus	CTAGTGTGG ACTCATCTGT YCTGATWATG AACCTKCARA TYAAGACMTA TGGTCAAGGC AGYGGGAATG CAGCC	1575
CEF94-BG.... ..G.... ..C....A... ..G..A.. ..T....C... ..C.....	1575
D6948-BT.... ..A.... ..T....T... ..T...G.. ..C....A... ..T.....	1575
Consensus	ACSTTCATCA ACAACCACT YYTKAGCACS CTWGTGCTWG ACCAGTGGAA CYTGATGARR CARCCYAGWC CAGAC	1650
CEF94-B	..G..... ..C.... ..CT.G.... ..G... ..A... ..T..... ..C..... ..GA ..G..C..A....	1650
D6948-B	..C..... ..T.... ..TC.T.... ..C... ..T.... ..A..... ..T..... ..AG ..A..T..T....	1650
Consensus	AGCGARGAGT TCAARTCAAT TGARGACAAG CTRGGYATCA ACTTYAAGAT TGAGAGGTCC ATTGATGAYA TYAGG	1725
CEF94-BG.... ..A.... ..G..... ..T.... ..T..... ..C..... ..T..... ..C...	1725
D6948-BA.... ..G..... ..A..... ..G..C.... ..C..... ..C..... ..C... ..T...	1725
Consensus	GGCAAGCTSA GACAGCTTGT CCYCCTTGCA CAACCAGGGT ACCTGAGTGG RGGGGTYGAA CCAGARCAAY CCAGC	1800
CEF94-BG.... ..T..... ..T..... ..T..... ..G.... ..T.... ..A... ..T...	1800
D6948-BC.... ..C..... ..C..... ..T..... ..A.... ..C.... ..G... ..C....	1800
Consensus	CCAACTGTWG AGCTKGACCT ACTWGGRTGG TCWGCWACWT ACAGCAAGA TCTYGGGATC TATGTGCCGG TGCTT	1875
CEF94-BT.... ..T.... ..A..G.... ..A..T..A... ..C..... ..C..... ..C....	1875
D6948-BA.... ..G.... ..C..A.... ..T..A..T... ..T..... ..T..... ..C....	1875
Consensus	GACAAGGAAC GCYTATTTTG YTCGTCTGCG TATCCCAARG GRGTAGAGAA YAARAGYCTC AARTCCAARG TYGGG	1950
CEF94-BC..... ..T..... ..T..... ..G.... ..A..... ..C..G..T... ..G....A... ..C...	1950
D6948-BT..... ..C..... ..A..... ..G.... ..T..A..C... ..A....G... ..T...	1950
Consensus	ATCGAGCARG CATACAARGT WGTCAAGTAY GAGGCGTTGA GGTGGTAGG TGGTTGGAAC TACCCACTCC TGAAC	2025
CEF94-BG.... ..G.... ..A..... ..T..... ..T..... ..T..... ..T..... ..T...	2025
D6948-BA.... ..A.... ..T..... ..T..... ..T..... ..T..... ..T..... ..T...	2025
Consensus	AAAGCTGCA AGAAYAAAGC ARGYGCWGCT CGGCGGCATC TGGAGGCCAA GGGGTTCCCR CTCGAYGAGT TCCTM	2100
CEF94-BC.... ..T...C... ..G.C..C... ..T..... ..T..... ..A..... ..C..... ..A	2100
D6948-BT.... ..C...T... ..A.T..A... ..T..... ..T..... ..G..... ..T..... ..C	2100
Consensus	GCCGAGTGGT CWGAGYTGT NGAGTTCGGW GARGCYTTCG AAGGCTTCAA YATCAAGCTG ACMGTAACAY CKGAG	2175
CEF94-BT...C... ..A..... ..T...G..C... ..T..... ..C..... ..T... ..T...	2175
D6948-BA...T... ..C..... ..A..A..T... ..T..... ..C..... ..A..... ..C... ..G...	2175
Consensus	AGCCTWCCG AACTKAACAR RCGATACCC CCCAARCCYC CAAATGTCAA CAGACCAGTC AACACYGGKG GRCFM	2250
CEF94-BA.... ..G.... ..A..G..... ..G...C... ..T..... ..T... ..G... ..A..C	2250
D6948-BC.... ..T.... ..G..A..... ..A..A..T... ..T..... ..C... ..T... ..G... ..A	2250
Consensus	AAGGCAGTCA GCAAYGCCCT CAAGACCGGY CGGTAYAGRA AYGAAGCCGG ACTRAGTGGY CTCGTCTYC TAGCC	2325
CEF94-BC..... ..T..... ..C...G... ..C..... ..G.... ..T..... ..T....	2325
D6948-BT..... ..T..... ..C..... ..T...A... ..T..... ..A.... ..C..... ..C....	2325
Consensus	ACMGCMGMA GCCGWCRTCA RGAYGCAGTY AAGGCCAAGG CAGARGCCGA GAACTCCAC AASTCYAAGC CMGAY	2400
CEF94-B	..A..AA.A... ..T...G... ..A..T... ..T..... ..A..... ..C..... ..A..C	2400
D6948-B	..C..CC.C... ..A..A... ..G..C.... ..C..... ..G..... ..T..... ..C... ..T	2400

Fig.2b Contd.		Alignment of IBV B-segment cDNA sequences									
Consensus	GACCCCGATG	CAGACTGGTT	YGAAMGRTCA	GAAACYCTGT	CAGACCTKCT	GGAGAAAGCC	GACATYGCCA	GCAAG	2475		
CEF94-B	C...A.A...T....T..C....	2475		
D6948-B	T...C.G...C....G..T....	2475		
Consensus	GTCGCTCACT	CAGCACTCGT	GGAAACAAGC	GACGCTCTTG	AAGCRGTYCA	GTCRACYTCM	GTGTACACYC	CMAAG	2550		
CEF94-BC....C....A..T..	...G..T..CT..	.C...	2550		
D6948-BT....T....G..C..	...A..C..AC..	.A...	2550		
Consensus	TACCCAGARG	TYAAGAACCC	ACAGACCGCC	TCCAACCCCG	TTGTTGGGCT	CCACCTGCCC	GCCAAGAGRG	CCACC	2625		
CEF94-BA..	.C.....A..	2625		
D6948-BG..	.T.....G..	2625		
Consensus	GGTGTCCAGG	CMGCTCTTCT	CGGAGCAGGR	ACGAGCAGAC	CAATGGGGAT	GGAGGCYCCA	ACACGGTCCA	AGAAC	2700		
CEF94-BC.....AC...	2700		
D6948-BA.....GT...	2700		
Consensus	GCCCTGAAAA	TGGCCAAMG	GCGGCAACGC	CAAAARGAGA	GCCGCCAAYA	GCCATGATGG	GAACCACTCA	AGAAG	2775		
CEF94-BC..G....C..	2775		
D6948-BA..A....T..	2775		
Consensus	AGGACACTAA	YCCAGACCC	CGTATCCCCG	GCCTTCGCCT	GCGGGGGCCC	CC			2827		
CEF94-B	T.....			2827		
D6948-B	C.....			2827		

Fig.3a IBDV polyprotein alignment

Consensus	MTNLQDOTQQ	IVPFIRSLIM	PTGPASIPD	DTLEKHTLRS	ETSTYNLTVG	DTGSGLIVFF	PGFPGSIVGA	HYTLQ	75
CEF94-PP	75
D6948-PP	75
TY89-PP	
Consensus	SNGNYKFDQM	LLTAQNLPAS	VNYCRLVSR	LTVRSSSTLPG	GVYALNGTIN	AVTFQGSLS	ETDVSYNGLM	SATAN	150
CEF94-PP	150
D6948-PP	150
TY89-PP	
Consensus	INDKIGNVLV	GEGVTVLSLP	TSYDLGVVRL	GDFIPAIGLD	PKMVATCDSS	DRFRVYTITA	ADDYQFSSQY	Q.GGV	225
CEF94-PP	225
D6948-PP	225
TY89-PP	
Consensus	TITLFSANID	AITSLS.GGE	LVPQTSV.GL	.LGATIYLLIG	FDGTAVITRA	VAA.NGLT.G	TDNL.PFN.V	IPT.E	300
CEF94-PP	300
D6948-PP	300
TY89-PP	
Consensus	ITQPITSIKL	EIVTSKSGGQ	AGDQMSWSA.	GSLAVTIHGG	NYPGALRPVT	LVAYERVATG	SVTVAGVSM	FELIP	375
CEF94-PP	375
D6948-PP	375
TY89-PP	
Consensus	NPFLAKNLVT	EYGRFPDGM	NYTKLILSER	DRLGIKTVPV	TREYTDFFREY	FMEVADLNSP	LKIAGAFGFK	DIIRA	450
CEF94-PP	450
D6948-PP	450
TY89-PP	
Consensus	.RRIAPVVS	TLFPPAAPLA	HAIGESVDYL	LGDEAQAASG	TARAASGKAR	AASGRIRQLT	LAADKGYEVV	ANLFQ	525
CEF94-PP	525
D6948-PP	525
TY89-PP	
Consensus	VFQNEVVVDGI	LASFG.LRGA	HNLCVLRREG	ATLFFVVVIT	VEDAMTPKAL	NSKMFVIEG	VREDLQPPSQ	RGSFI	600
CEF94-PP	600
D6948-PP	600
TY89-PP	
Consensus	RTLSGHRVYG	YAPDGLVPLE	TGRDYTVVPI	DDVWDDSIML	SKDPIPIVIG	NSGNLAIAYM	DVFRPKVPIH	VAMTG	675
CEF94-PP	675
D6948-PP	675
TY89-PP	
Consensus	ALNA.GEIE.	VSFRSTKLAT	AHRLGLKLAG	PGAFDVNTG.	NWATFIKREF	HNPRDWRDLP	YLNLEPLPPN	AGROY	750
CEF94-PP	750
D6948-PP	750
TY89-PP	28
Consensus	HLAMAASEFK	ETPELESAYR	AMEAAANVDP	LFQSALSVMF	WLEENGIVTD	MANFALSDPN	AHRMRNPLAN	APQAG	825
CEF94-PP	825
D6948-PP	825
TY89-PP	103
Consensus	SKSQRAKYGT	AGYGVVEARGP	TPEEAQREKD	TRISKMETM	GIYFATPEWV	ALNGHRGSPSP	GQLKYWQNT	EIPDP	900
CEF94-PP	900
D6948-PP	900
TY89-PP	178
Consensus	NEDYLDVYHA	EKSRLASEBQ	ILRAATSIYG	APGQAEPPQA	FIDEVAKVYE	INHGRGPNQE	QMKDLLELTAM	EMKHR	975
CEF94-PP	975
D6948-PP	975
TY89-PP	253
Consensus	NPRRAPPKPK	PKPNAPTQRP	PGRLGRWIRT	VSEDELE					1012
CEF94-PP					1012
D6948-PP					1012
TY89-PP					290

Fig.3b IBDV VP1 alignment

Consensus	MSD.FNSPQA RS.ISAAPGI KPTAGQDVEE LLIPKVVVFP EDPLASPSRL AKFLRENGYK .LQPRSLPEN EEEYET	75
CEF94-VP1	...I.....T.....V.....	75
D6948-VP1	...V.....K.....I.....	75
Consensus	DQILPDLAWM RQIEGAVLKP TSLPFGDQE YFPKYPTTHR PSKEKNAYP PDIALLKQMI YLFLQVPEA. .LKD	150
CEF94-VP1N EG...	150
D6948-VP1T DN...	150
Consensus	EVTLTQNIR DKAYGSGTYM GQATRLVAMK EVATGRNPKN DPLKLGTYFE SIAQLLDITL PVGPPGEDDK FMVPL	225
CEF94-VP1	225
D6948-VP1	225
Consensus	TRVPSRMLVL TGDVDG.FEV EDYLPKINLK SSSGLPYVGR TKGETIGEMI AISNQFLREL S.LLKQGACT KGSNK	300
CEF94-VP1D.....T.....	300
D6948-VP1E.....A.....	300
Consensus	KKLLSMLSDY WYLSGGLLFP KAERYDKSTW LTRTRNIWSA PSPHLMISM ITWPVMSNSP NNVLNIEGCP SLYKF	375
CEF94-VP1	375
D6948-VP1	375
Consensus	NPFGRGLNRI VEWI.AP.EP KALVYADNIY IVHSNTWYSI DLEKGEANCT RQHMQAAMYI ILTRGWSNNG DPMFN	450
CEF94-VP1L..E.....	450
D6948-VP1M..D.....	450
Consensus	QTWATFAMNI APALVVDSSC LIMNLQIKTY GQGSGNAATF INNHLSTLV LDQWNL.M.QP .PDSEEFKSI EDKLG	525
CEF94-VP1R.. R.....	525
D6948-VP1K.. S.....	525
Consensus	INFKIERSID DIRGKLRQLV .LAQPGYLSG GVEPEQ.SPT VELDLLGWSA TYSKDLGIYV PVLDERLFC SAAYP	600
CEF94-VP1L.....S.....	600
D6948-VP1P.....P.....	600
Consensus	KGVENKSLKS KVGIEQAYKV VRYEALRLVG GWNYPLLNKA CIGNA.AARR HLEAKGFPLD EFLAEWSELS EFGEA	675
CEF94-VP1G.....	675
D6948-VP1S.....	675
Consensus	FEQFNKLTIV T.ESLAEIN. PVFPKPPNVN RPNVTGGLKA VSNALKTGRY RNEAGLSGLV LLATARSRLQ DAVKA	750
CEF94-VP1S.....K.....	750
D6948-VP1P.....R.....	750
Consensus	KAAEAKLHKS KPDDPDADWF ERSETLSDLL EKADIASKVA HSALVETSDA LEAVQSTSVY TPKYPEVKNP QTASN	825
CEF94-VP1	825
D6948-VP1	825
Consensus	PVVGHLHPAK RATGVQAALL GAGTSRPMGM EAPTRSKNAV KMAKRRQRQK ESQ..	881
CEF94-VP1QP	881
D6948-VP1--	879

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Fig. 3c IBDV VP5 alignment

Consensus	MVSRDQTNDR SDD.PARSNP TDCSVHTEPS DANNRTGVHS GRHP.EAHSQ	50
D6948-VP5E.....R.....	50
CEF94-VP5K.....G.....	50
Consensus	VRDLDLQFDC GGHRVRANCL FPW.FWLNCG CSLHTAEQWE LQVRSDAPDC	100
D6948-VP5F.....	100
CEF94-VP5I.....	100
Consensus	PEFTGQLQLL QASESESHSE VKHT.WWRLC TK.HMKRRDL PRKPE	145
D6948-VP5P.....W.....	145
CEF94-VP5S.....R.....	145

20470-7299-001

Fig. 4 Schematic representation of the used plasmids

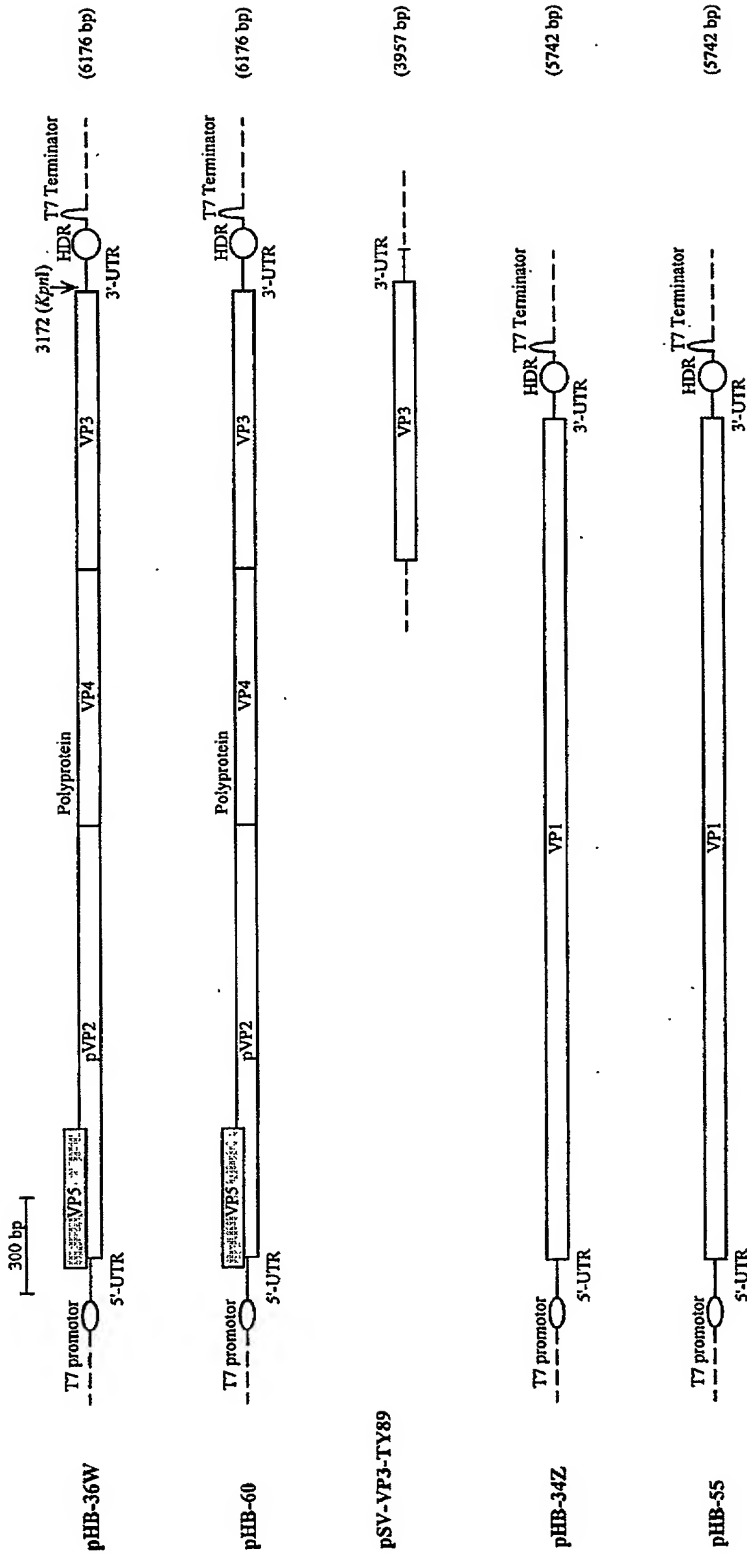


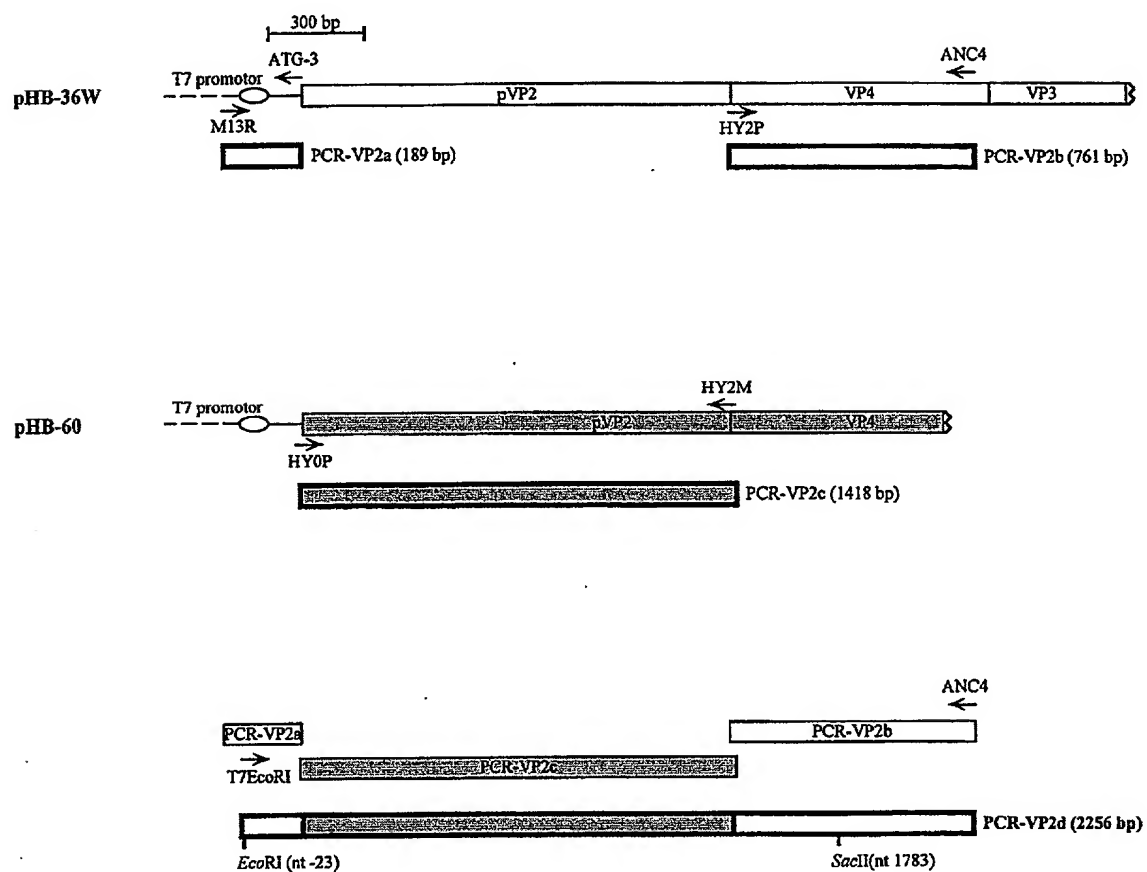
Fig. 5a Schematic representation of the construction of PCR fragment PCR-VP2d

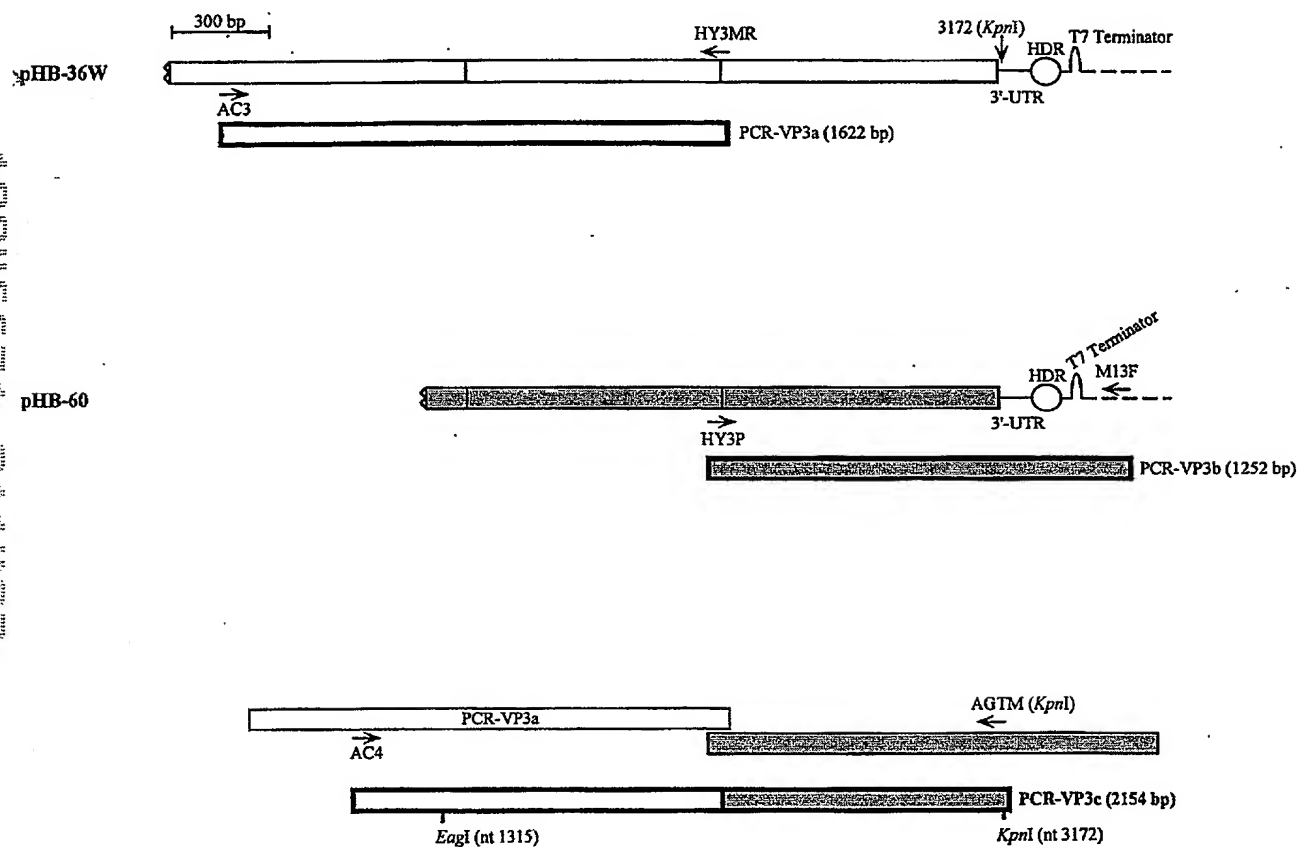
Fig. 5b Schematic representation of the construction of PCR fragment PCR-VP3c

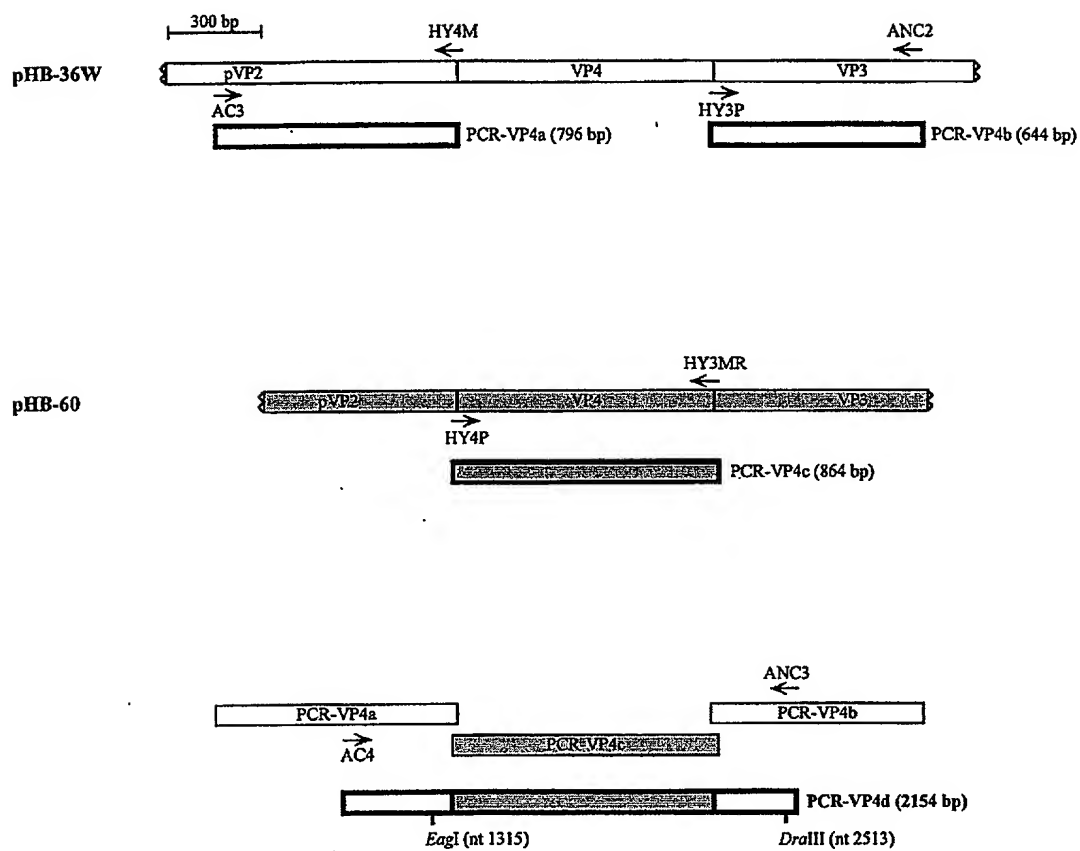
Fig. 5c Schematic representation of the construction of PCR fragment PCR-VP4d

Fig. 5d Schematic representation of the construction of plasmid pHB36-s2VP3

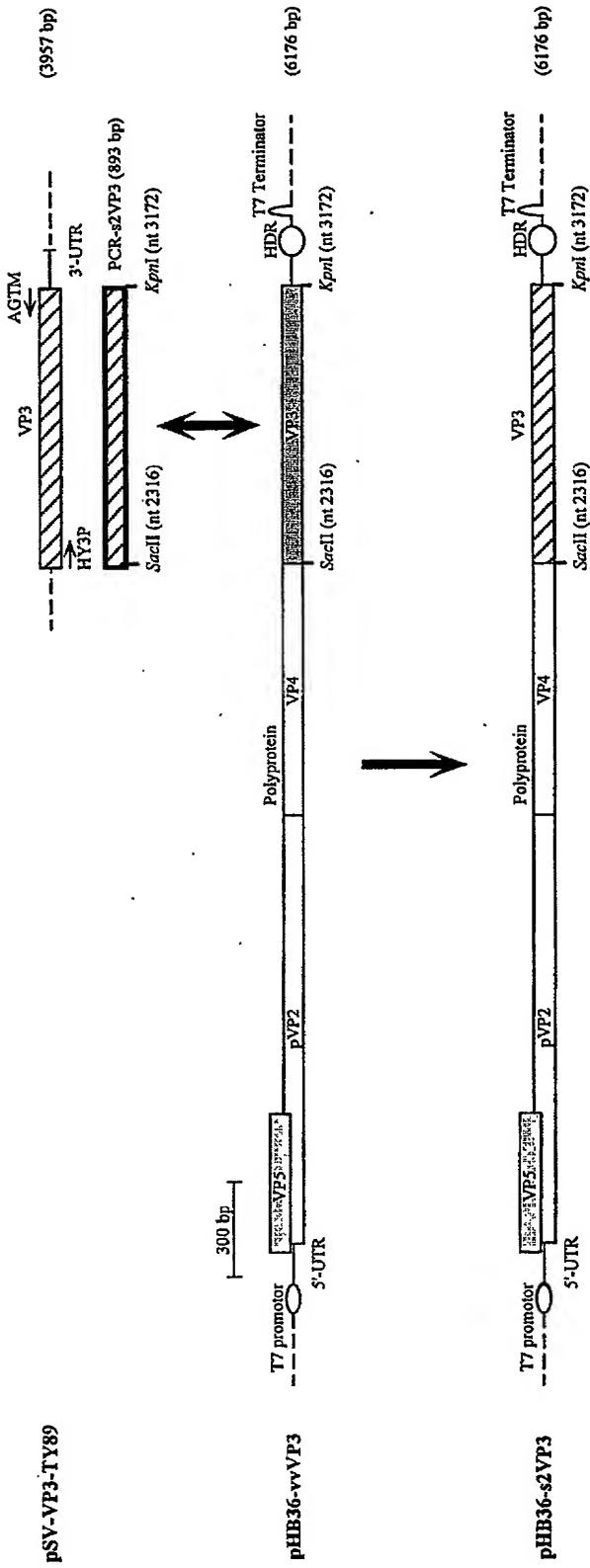


Fig. 5e Schematic representation of the construction of plasmid pHB36-s2VP3C

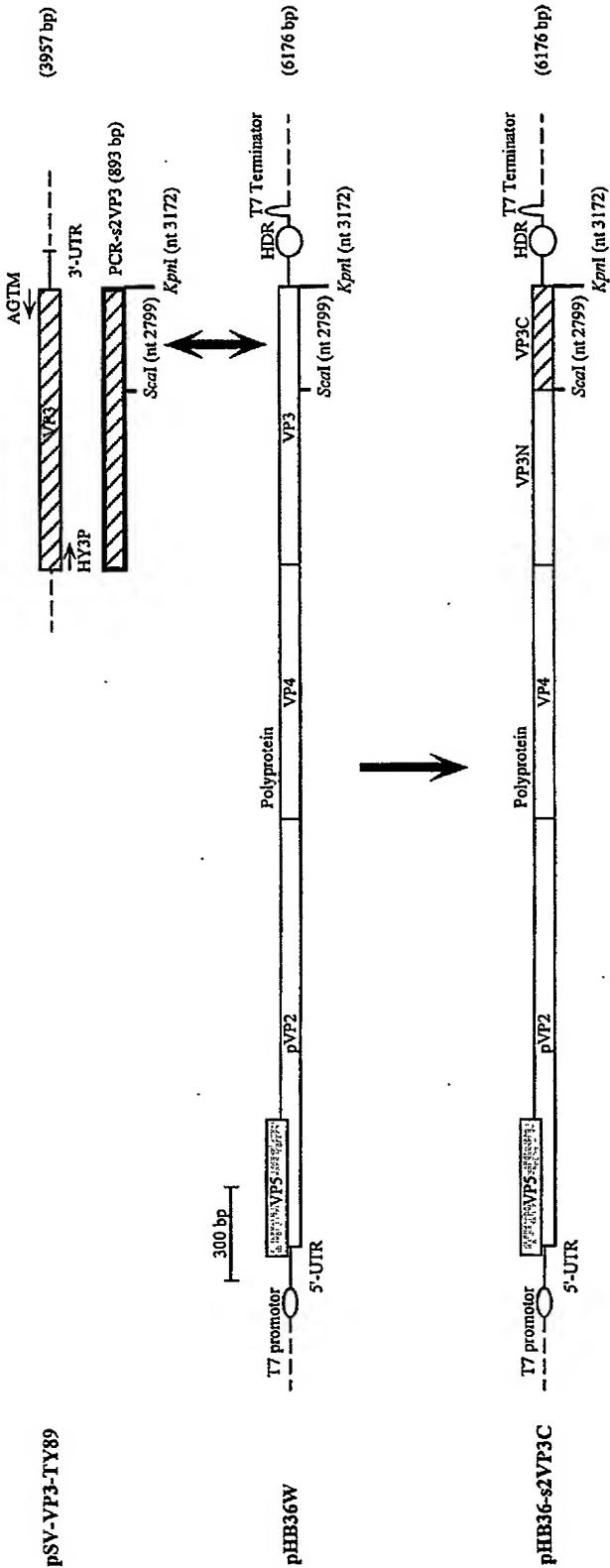


Fig. 5f Schematic representation of the construction of plasmid pHB36-s2VP3N

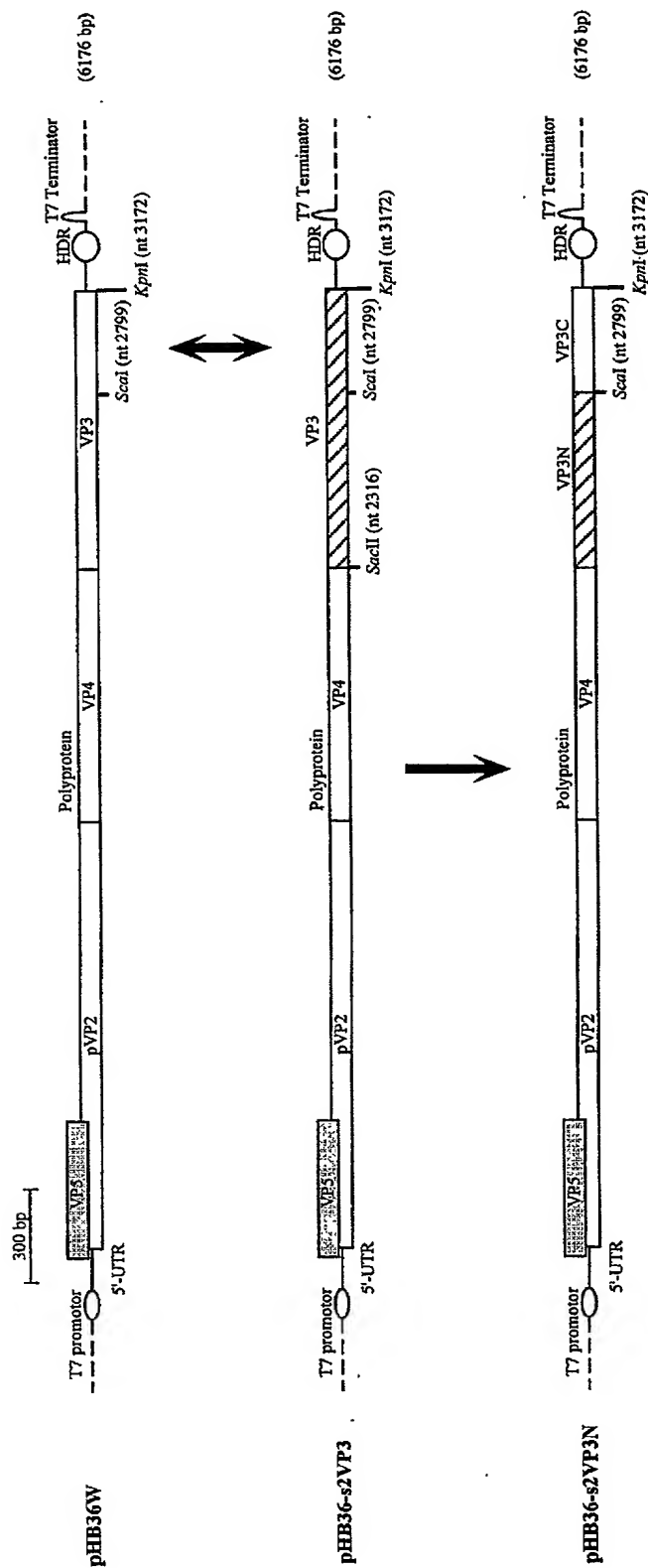
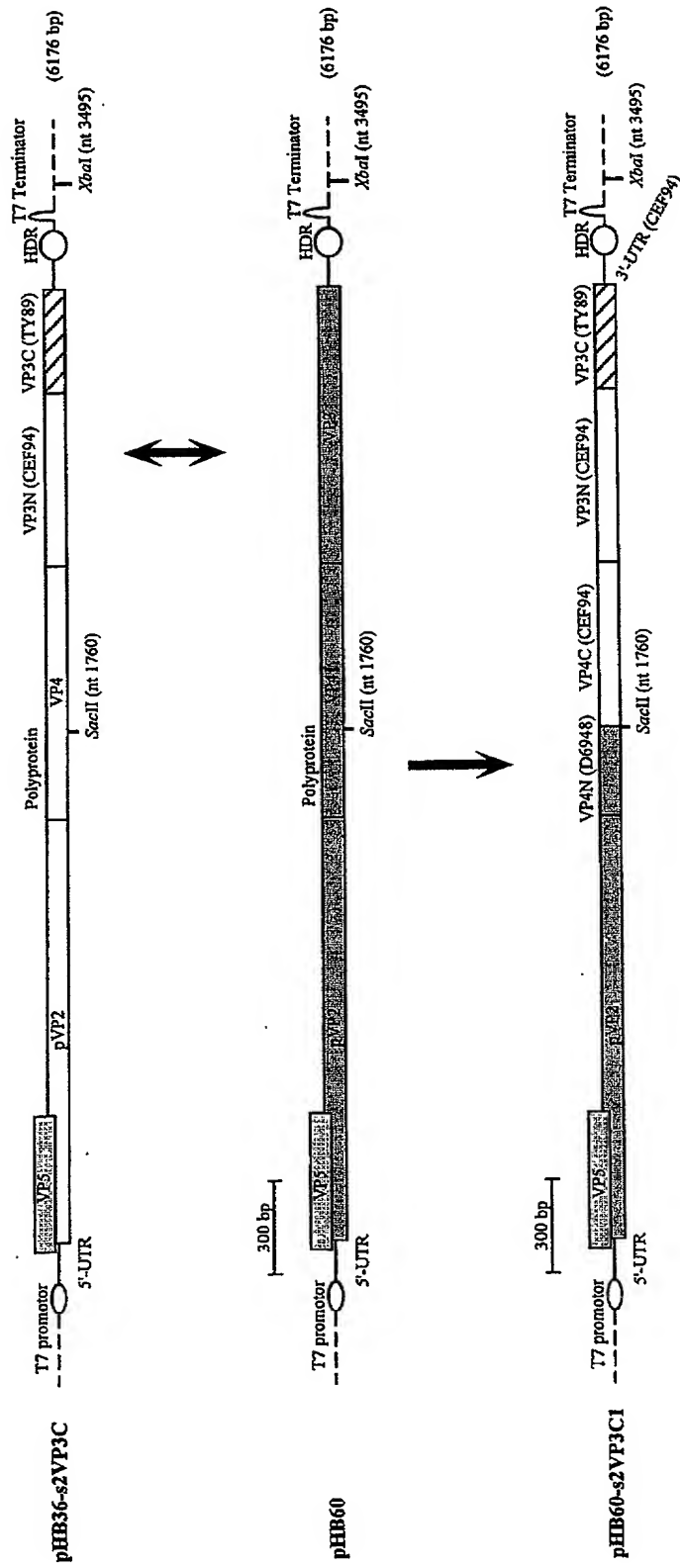
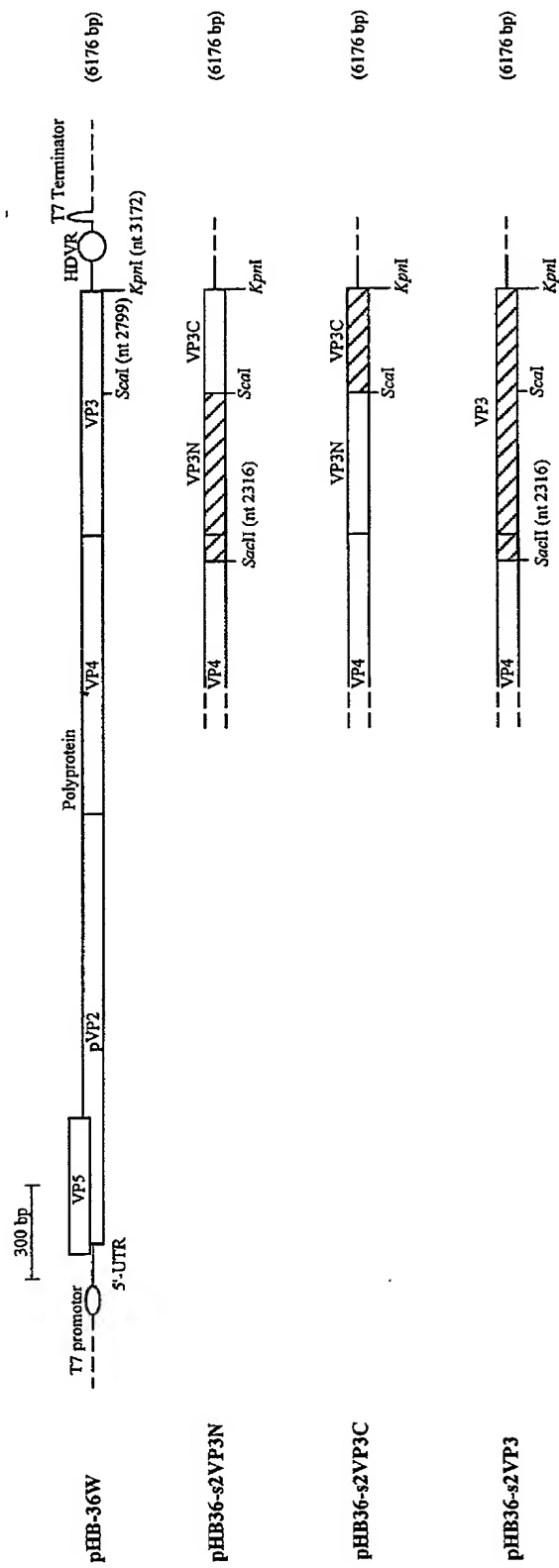


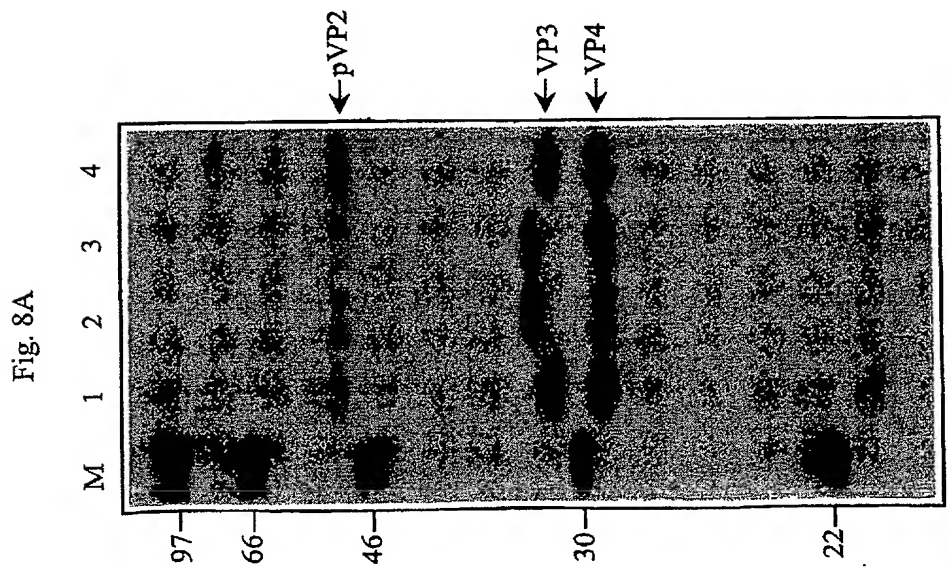
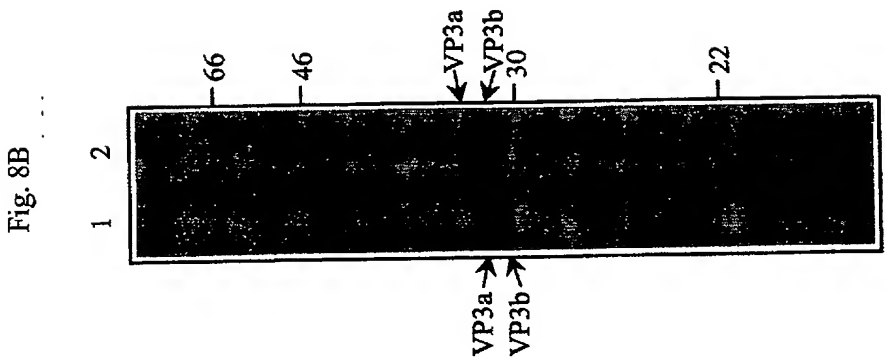
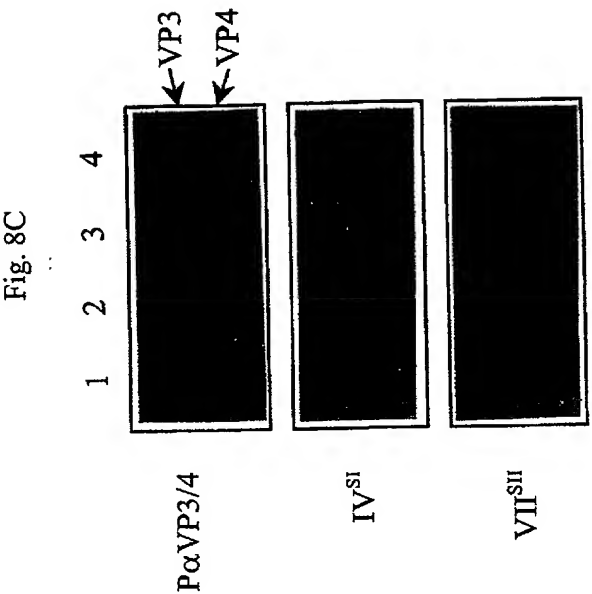
Fig. 5g Schematic representation of the construction of plasmid pHB60-s2VP3C1



[illegible]

Fig. 7





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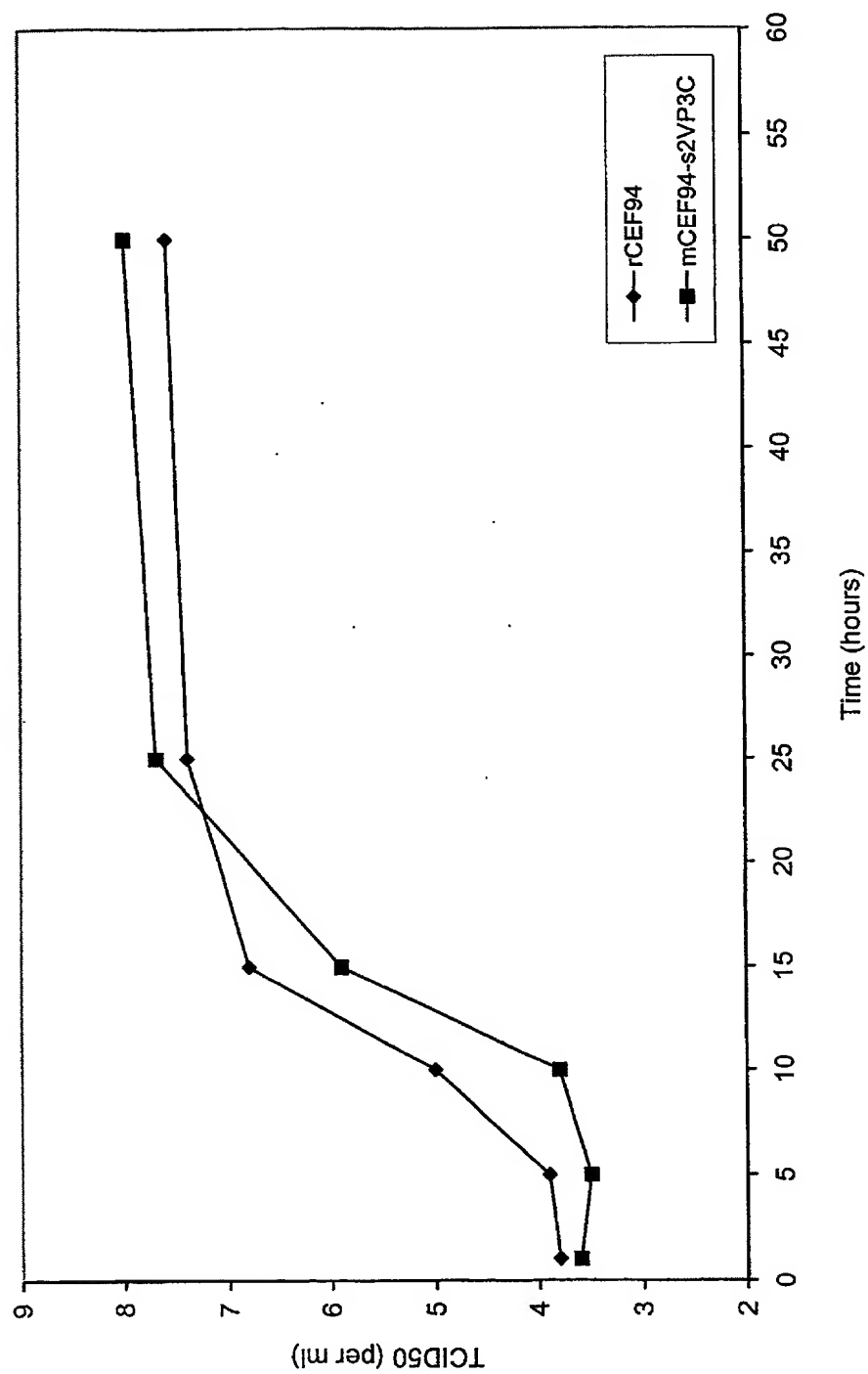
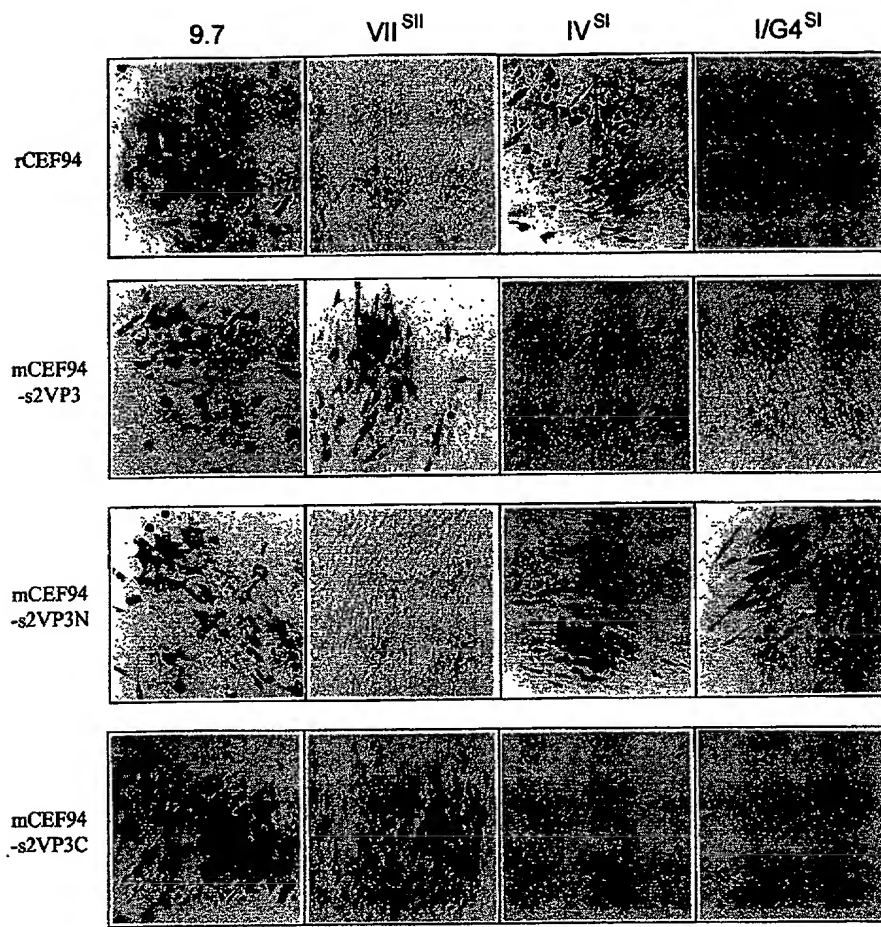


Fig. 9

Fig. 10



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Fig. 11

Schematic representation of plasmids pHB60-s2VP3C1 and pHB60-s2VP3C3

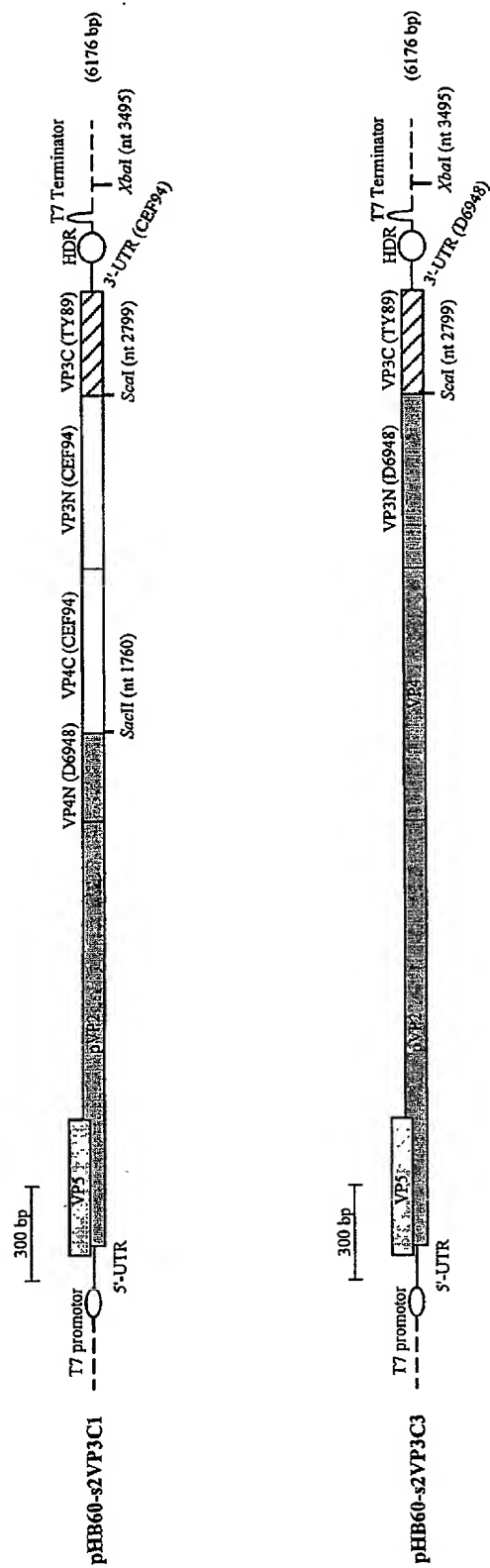
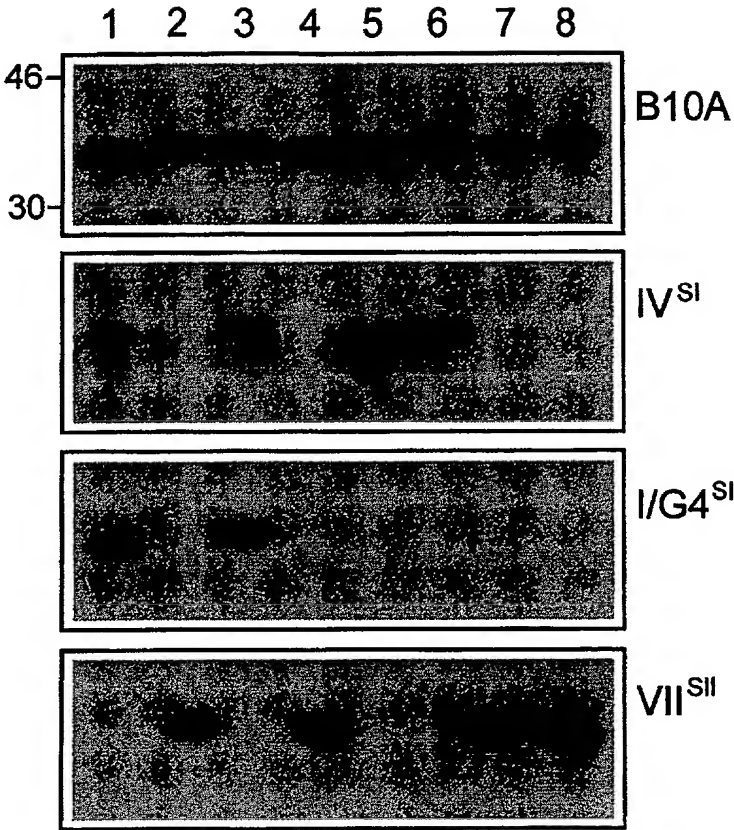


Fig. 12



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Fig. 13

		VP4 ← VP3	
CEF94-PP D6948 TY89-PP	724-FPHNPRD	WDRLPYLNL	YLPNAGRQY HLAWAASEFK ETEPLESAVR AMEAAANVDP LFQSALSVM WLEENGIVTD 800
	724-.....D
	724-.....T.....F.....L.....D.....R...Q... 800
CEF94-PP D6948 TY89-PP	MANFALSDPN	AHMRNFIAN	APQAGSKSOR AKYGTAGYGV EARGTPPEEA QREKDTIRISK KMETWGIYFA TPEWVALNGH 880
K.....

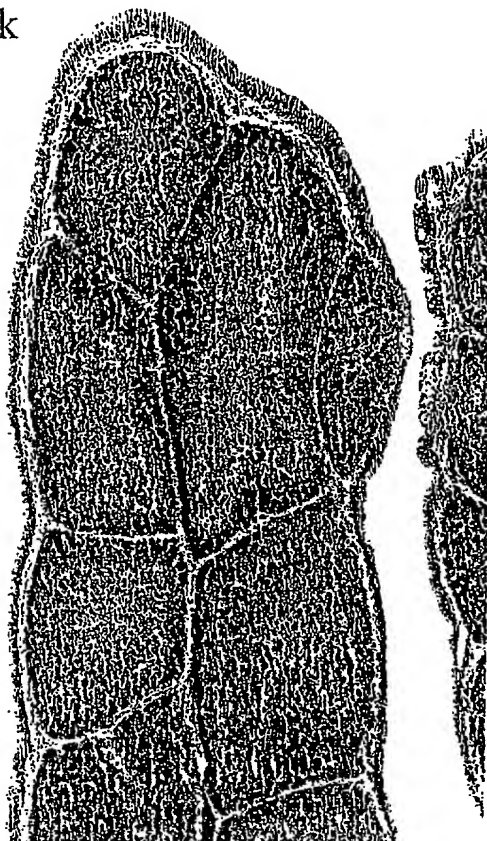
CEF94-PP D6948 TY89-PP	RGPSPGQLKY	WONTREIPDP	NEDYLDYVHA EKSRLASEEQ ILRAATSIYG APGQAEPPQA FIDEVAKVYE INHGRGNQE 960
E.....V.....R... 960

CEF94-PP D6948 TY89-PP	QMKDILLITAM	EMKHRNPRRA	LPKPKPKPNA PTQRPGRGLG RWIRTVSDDE LE 1012
P.....A..... 1012
P.....S..... 1012

SacII

ScaI

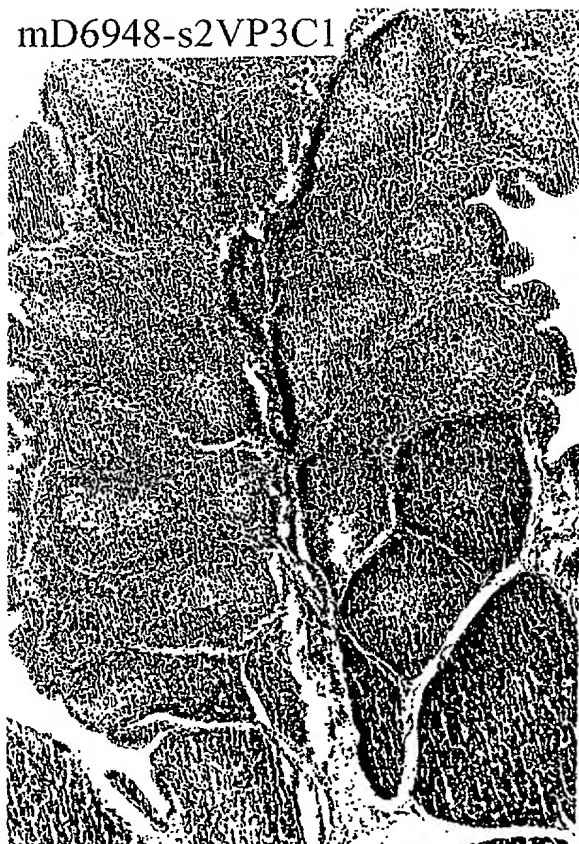
Mock



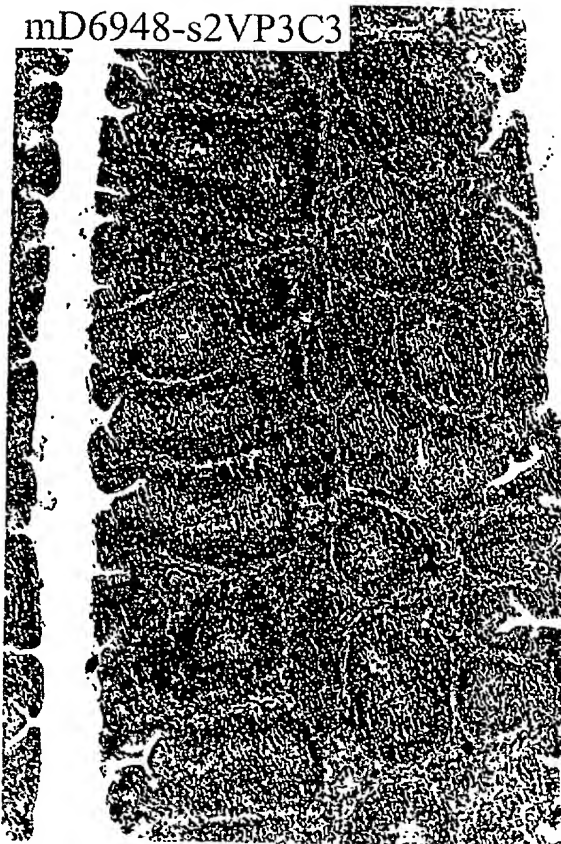
D6948



mD6948-s2VP3C1



mD6948-s2VP3C3



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FIG. 15

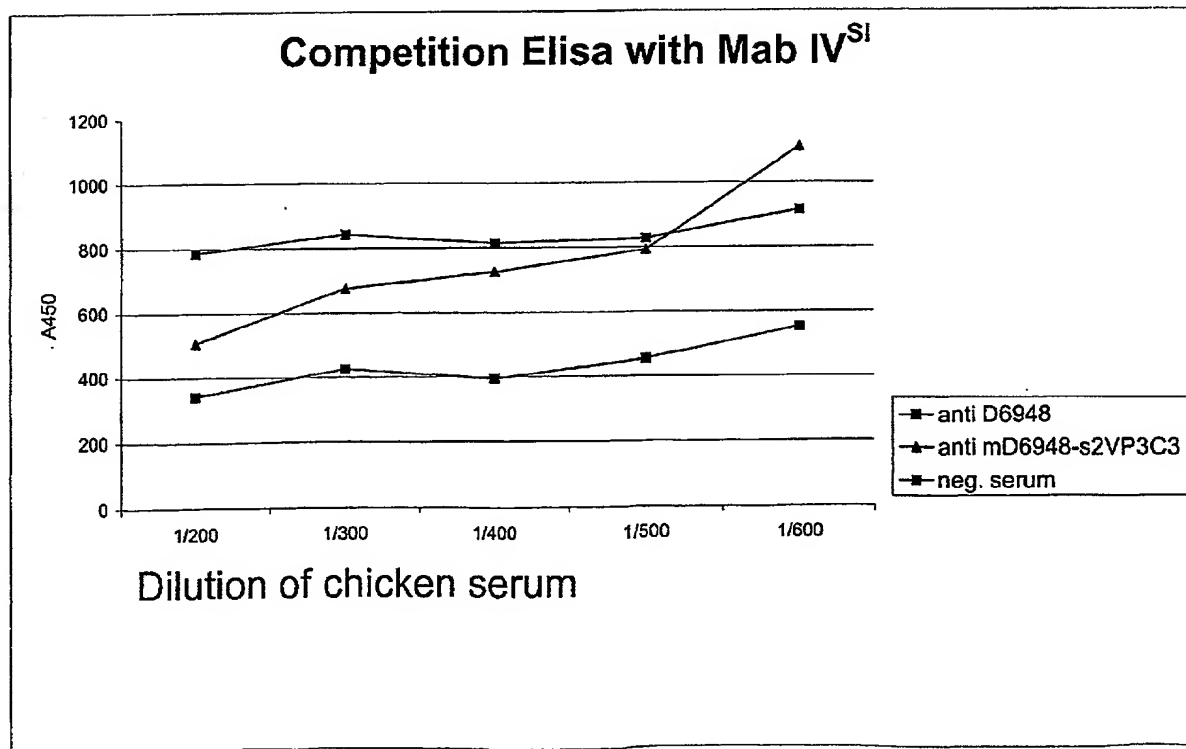
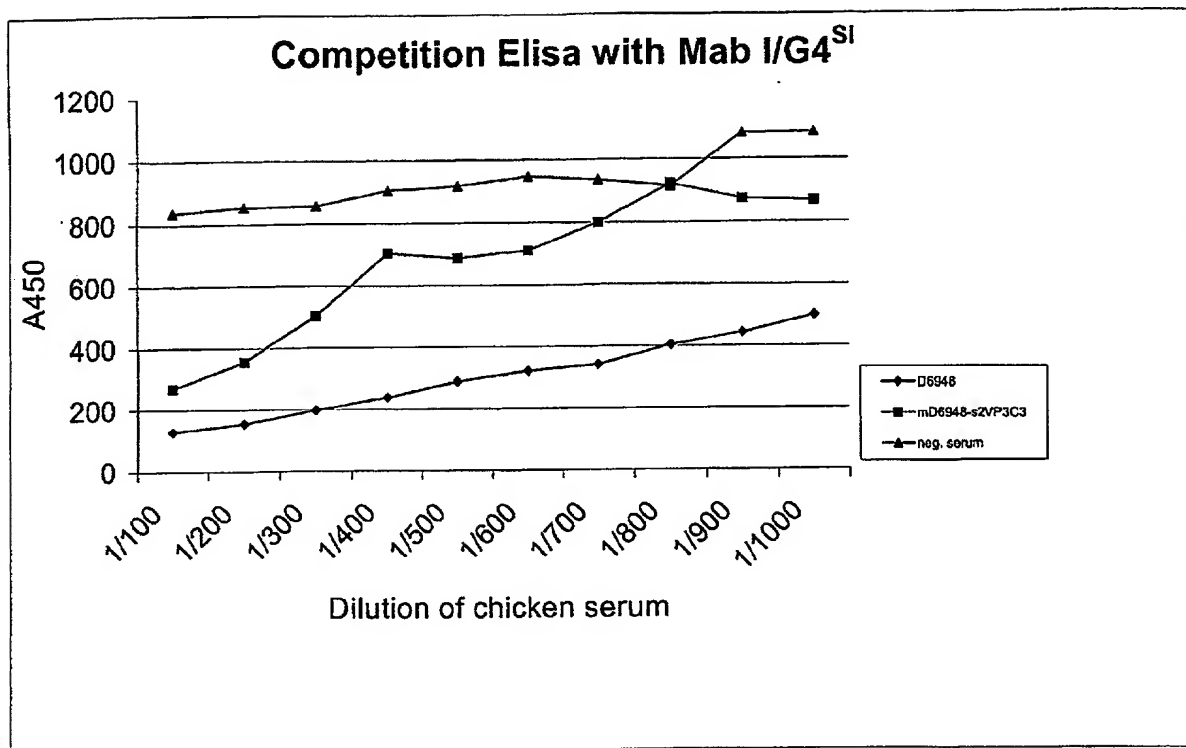


Fig. 16A

D6948-VP5	MLSLMVSRDQ	TNDRSDDEPA	RSNPIDCSVH	TEPSDANNRT	GVHSGRHPRE	AHSQVRDLDL	QFDCGGHVR	ANCLF	75
CEF94-VP5	----		K		G				71
	PWFPWLNCGC	SLHTAEQWEL	QVRSDAPDCP	EPTGQLQLLQ	ASESESHSEV	KHTPWNRIC	KWHKRRDLP	RKPE	149
	I				S		R		145

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Fig. 16B

D6948-PP	MTNLQDQTQQ	IVPFIRSLIM	PTTGPASIPD	DTLEKHTLRS	ETSTYNLTVG	DTGSLIVFF	PGFPGSIVGA	HVTLQ	75
CEF94-PP	SNGNYKFDQM	LLTAQNLPAS	YNYCRLVSR	LTVRSTLPG	GVYALNGTIN	AVTFQGSLS	LTDVSYNGLM	SATAN	150
	INDKIGNVLV	GEQVTVLSLP	TSYDLGYVRL	GDPIPAIGLD	PKMVAICDSS	DRPRVYTITA	ADDYQFSSQY	QAGGV	225
	TITLFSANID	AITSLSIGGE	LVFQTSVQGL	ILGATTIYLIG	PDGTAVITRA	VAADNGLTAG	TDNLMFPNIV	IPITSE	300
	ITQPITSIKL	EIVTSKSGGQ	AGDQMSWSAS	GSLAVTIHGG	NYPGALRPVT	LVAYERVATG	SVVTVAGVSN	FELIP	375
	NPELAKNLVT	EYGRFDPGAM	NYTKLILSER	DRLGIKTVP	TREYTDREY	FMEVADLNSP	LKIAGAFGFK	DIIRA	450
	LRRIAIPVVS	TLFPPAAPLA	HAIGEGVDYL	LGDEAOAASG	TARAASGKAR	AASGRIROLT	LAADKGYEVV	ANLFO	525
	VPONPVVDGI	LASPGILRGA	HNLDVLRREG	ATLEFPVITT	VEDAMTPKAL	NSKMFVIEG	VREDLOPPSO	RGSFI	600
	RTLSGHRVYG	YAPDGVLPLE	TGRDYTVVPI	DDVWDDSIML	SKDPIPIVIG	NSGNLAIAYM	DVFRPKVPIH	VAMTG	675
	ALNAYGEIEN	VSRSTKLAT	AHRLGLKLAG	PGAFDVNTGS	NWATFIKRP	HNPRDWDRLP	YLNLPYLPN	AGRQY	750
	DLAMAASEFK	ETPELESVR	AMEAAANVDP	LFQSALSVM	WLENGIVTD	MANFALSDPN	AHRMRNFLAN	APQAG	825
	SKSORAKYGT	AGYGVVEARGP	TPEEAQREKD	TRISKWEIM	GIYFATPEW	ALNGHRGPSP	GQLKYWQNT	EIPDP	900
	NEDYLDYVHA	EKSRLASEEQ	ILRAATSIYG	APQAEPPQA	FIDEVAKVYE	INHGRGNQE	QMKDLLLTAM	EMKHR	975
	NPRRAPPKPK	PKPNAPTQRP	PGRIGRWIRA	VSEDELE					1012

Fig. 16C

D6948-VP1	MSDVFNPOA	RSKISAAFGI	KPTAGQDVEE	LLIPKVVVPP	EDPLASPSRL	AKFLRENGYK	ILQPRSLPEN	EEYET	75
CEF94-VP1	I	T				V			
	DQILPDLAWM	RQIEGAVLKP	TLSLPICDQE	YFPKYYPTHR	PSKEKPNAYP	PDIALLKQMI	YLFLOVPEAT	DNLKD	150
						N	EG		
	EVTLLTONIR	DKAYSGTYM	GQATRLVAMK	EVATGRPNPK	DBLKLGTYFE	SIAQLLDITL	PVGPPGEDDK	PWVPL	225
	TRVPSRMLVL	TGDVDGEFEV	EDYLPKINK	SSSGLPYVGR	TKGETIGEMI	AISNQFLREL	SALLKQGAGT	KGSNK	300
		D				T			
	KKLLSMLSDY	WYLSGGLLFP	KAERYDKSTW	LTKTRNIWSA	PSPTHLMISM	ITWPVMSNSP	NNVLNIEGCP	SLYKF	375
	NPFRGGLNRI	VEWIMAPDEP	KALVYADNIY	IVHSNTWYSI	DLEKGEANCT	RQHMQAAMYY	ILTRGWSDNG	DPMFN	450
		L	E						
	QTWATFAMNI	APALVVDSSC	LIMNLQIKTY	GQSGNAATF	INNHLISTLV	LDQWNLMKQP	SPDSEEFKSI	EDKLG	525
						R	R		
	INFKIERSID	DIRGKLRQLV	PLAQPGLYLSG	GVEPEQPSPT	VELDLLGWSA	TYSKDLGIYV	PVLDKERLFC	SAAYP	600
		L		S					
	KGVENKSLKS	KVGIEQAYKV	VRYEALRLVG	GWNYPLLNKA	CKNNASAARR	HLEAKGFPLD	EFLAEWSELS	EFGEA	675
					G				
	FEFENIKLTV	TPESLAEINR	PVPPKPPNVN	RPVNTGGLKA	VSNALKTGRY	RNEAGLSGLV	LLATARSRLQ	DAVKA	750
		S	K						
	KAAEAKLHKS	KPDDPDADWF	ERSETLSDLL	EKADIASKVA	HSALVETSDA	LEAVQSTSVY	TPKYPEVKNP	QTASN	825
	PVVGLHLPK	RATGVQAALL	GAGTSRPMGM	EAPTRSKNAV	KMAKRRQRQK	ESRQ--			879
						QP			881

Fig. 17

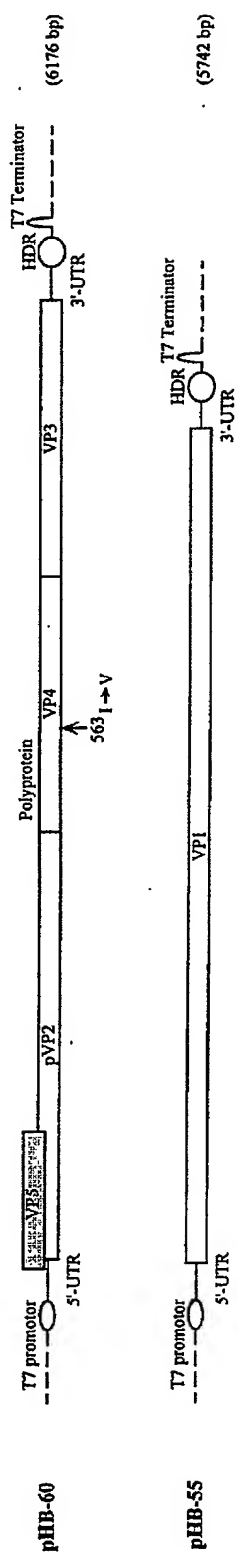


Fig. 18a

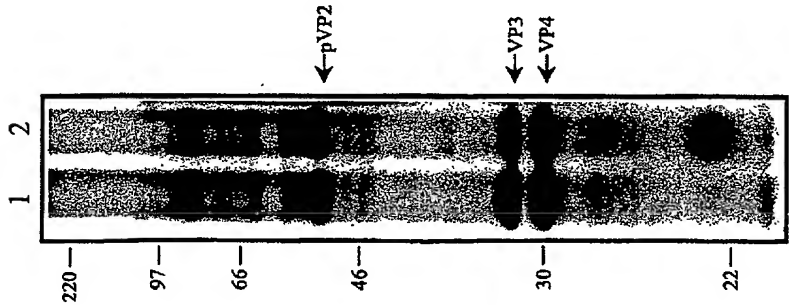


Fig. 18b

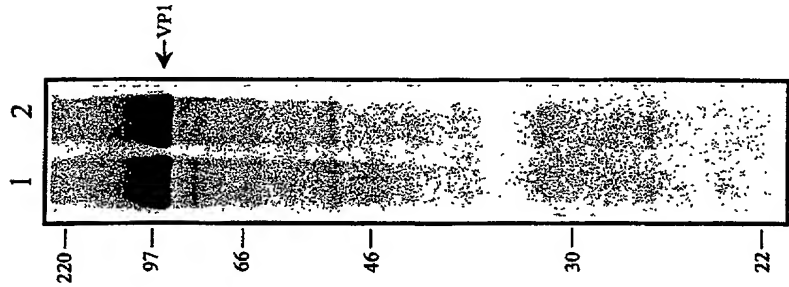


Fig. 18c

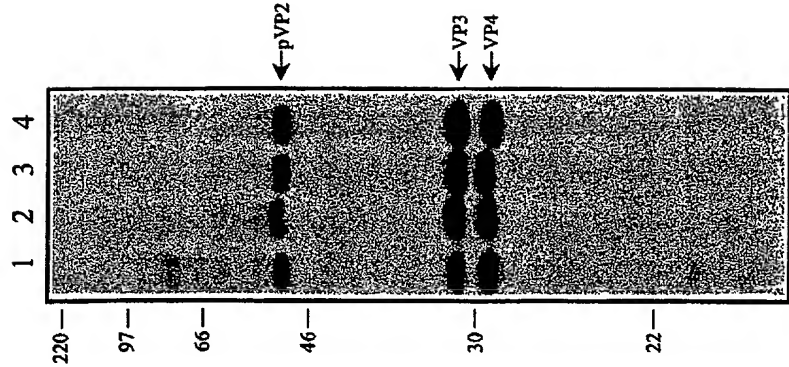
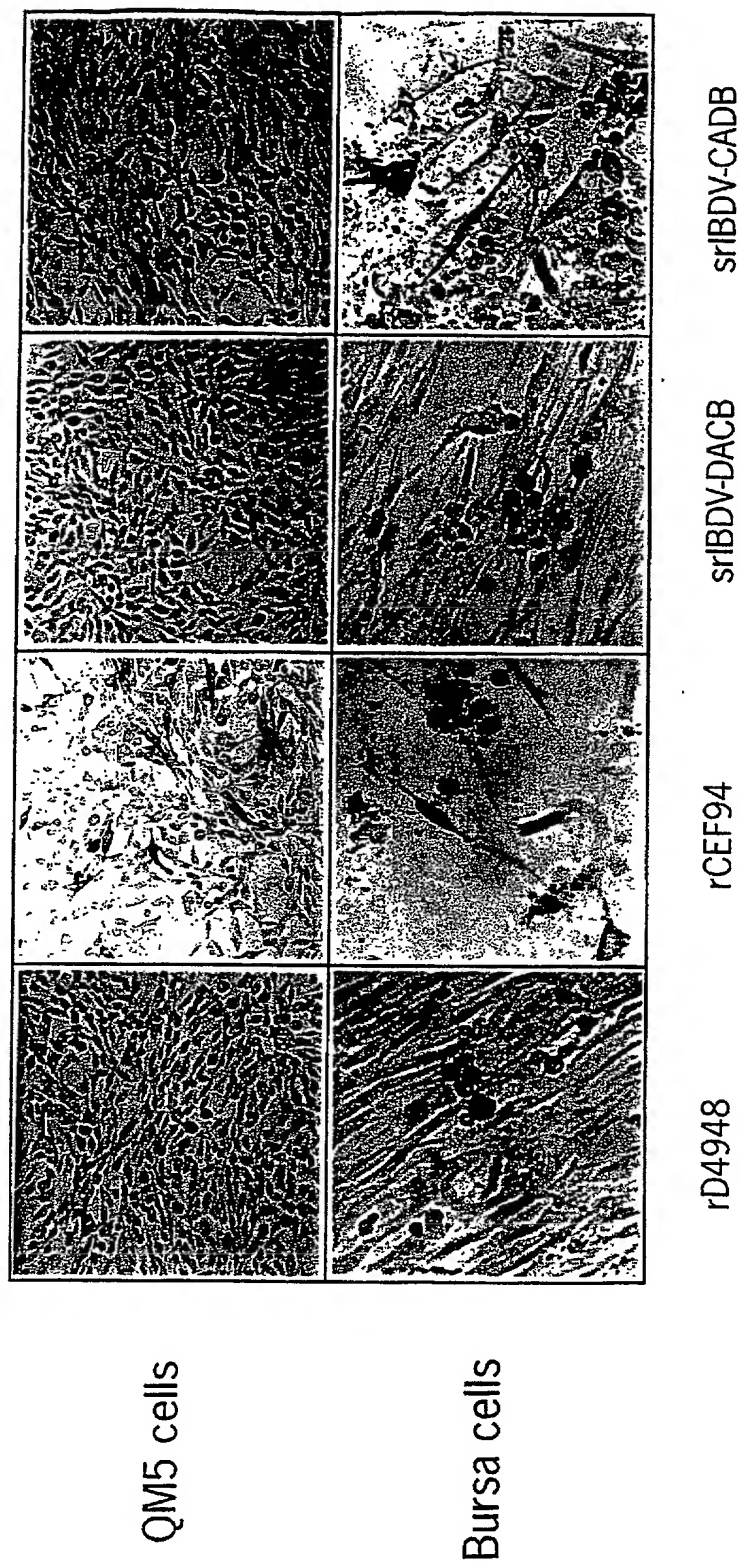


Fig. 19



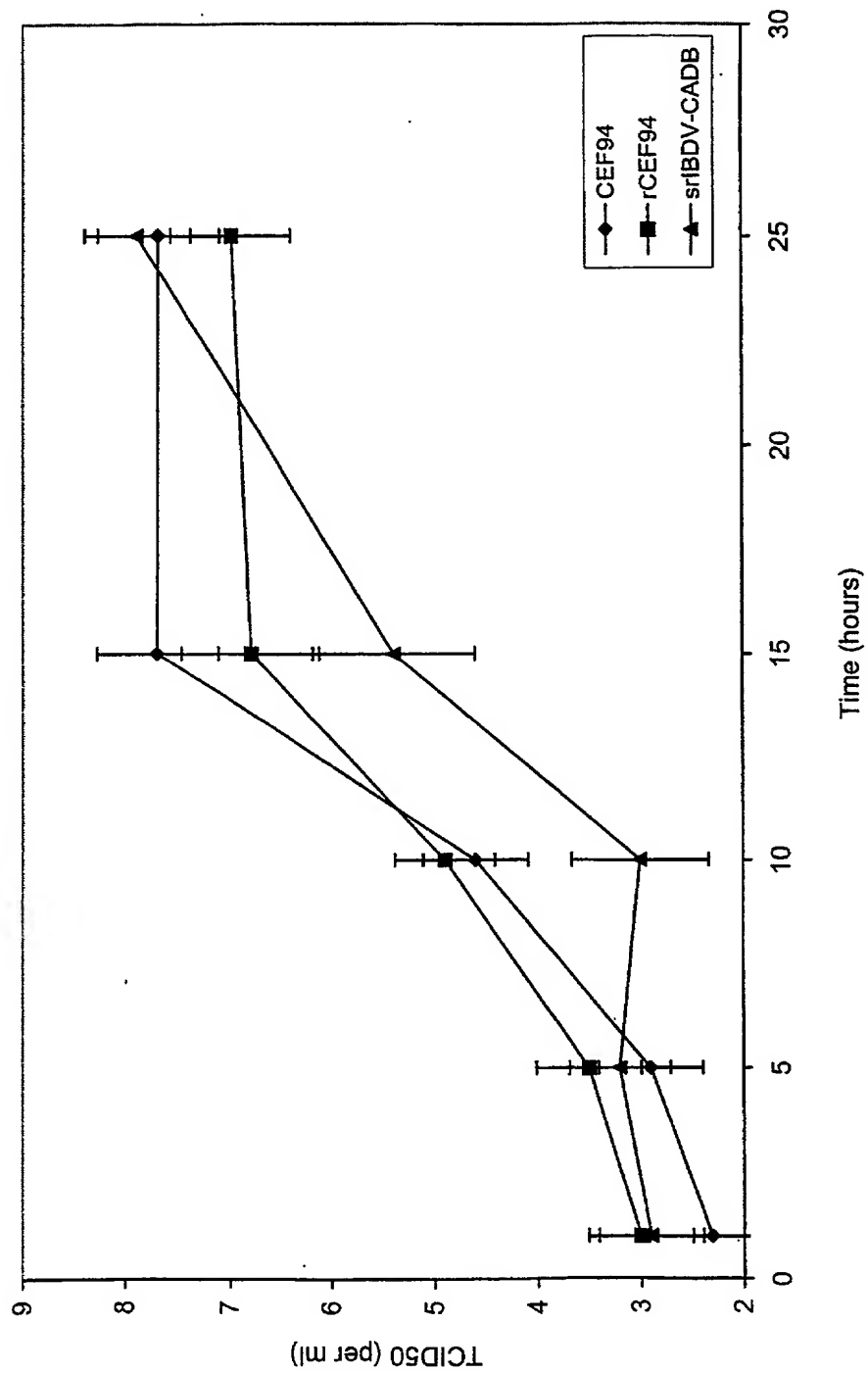


Fig. 20

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Fig. 21

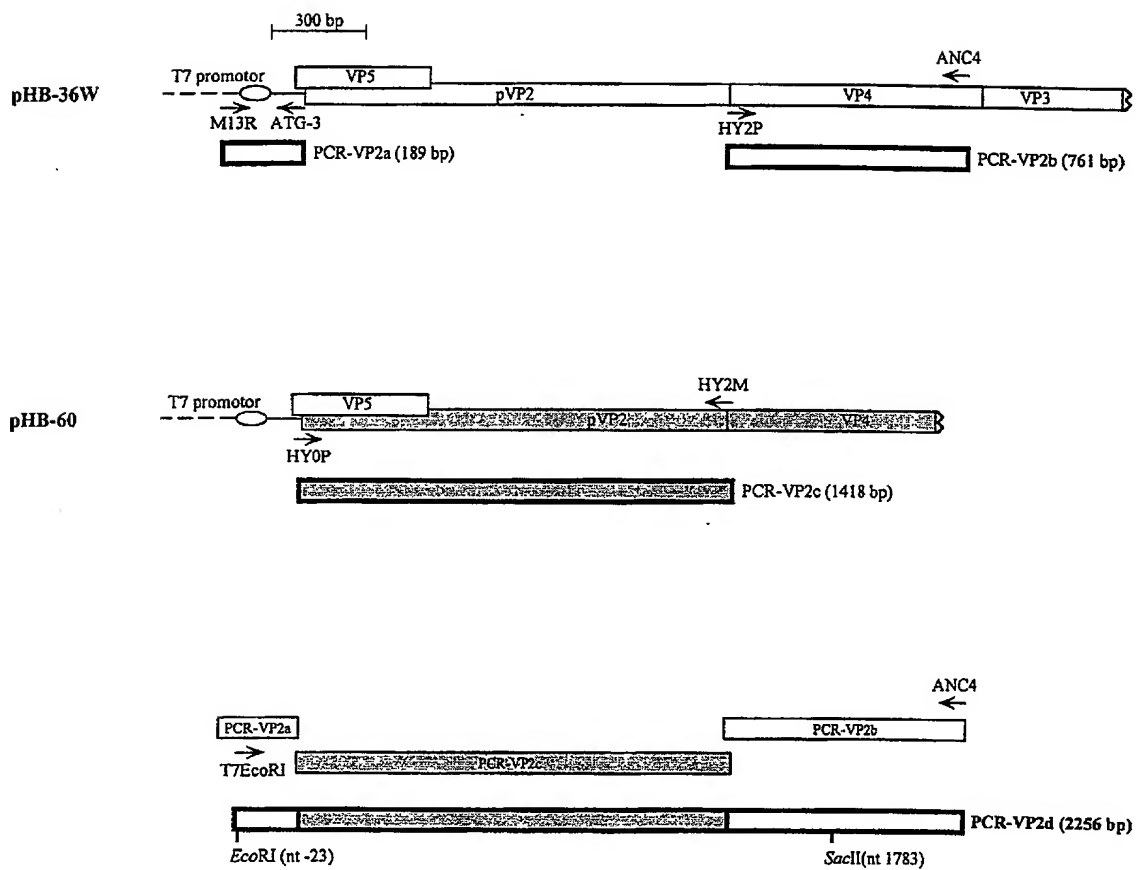


Fig. 22

